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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:02 ; Search time 10.338 Seconds

(without alignments)  
1055.158 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357

Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALLKYVNGTCQCT 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1096.5	80.8	261	1	RIP3.PHYAM
2	1050	77.4	313	1	RIP1.PHYAM
3	1014.5	74.8	294	1	RIP1.PHYAM
4	453	33.4	310	1	RIP2.PHYAM
5	342	25.2	299	1	RIP6.SAPOR
6	337	24.8	253	1	RIP5.SAPOR
7	336	24.8	253	1	RIP7.SAPOR
8	335.5	24.7	292	1	RIP2.SAPOR
9	319.5	23.5	293	1	RIP0.DIACA
10	313	23.1	316	1	RIP3.GELMU
11	291	21.4	576	1	RIC1.RICCO
12	287.5	21.2	294	1	RIP1.TRIAN
13	283	20.9	236	1	RIP3.SAPOR
14	271.5	20.0	564	1	AGGL.RICCO
15	260	19.2	282	1	RIP2.BRYDI
16	257	18.9	278	1	RIP1.MIRJA
17	250	18.4	286	1	RIP1.CUCPT
18	247.5	18.2	286	1	RIP1.MOMCH
19	241	17.8	289	1	RIP5.TRIKI
20	240	17.7	289	1	RIP1.TRIKI
21	235	17.3	250	1	RIPB.LUCFY
22	233.5	17.2	563	1	NIGB.SAMNI
23	230.5	17.0	528	1	ABRA.ABRPR
24	229	16.9	527	1	ABRA.ABRPR
25	225	16.6	290	1	RIP1.BRYDI
26	215	15.8	286	1	RIP2.MOMBA
27	209.5	15.4	562	1	ABRC.ABRPR
28	200	14.7	254	1	MLA.VISAL
29	199.5	14.7	277	1	RIP4.LUCFY
30	199.5	14.7	277	1	RIP4.SAPOR
31	199.5	14.7	277	1	RIP4.SAPOR
32	199.5	14.7	277	1	RIP4.SAPOR
33	199.5	14.7	277	1	RIP4.SAPOR
34	199.5	14.7	277	1	RIP4.SAPOR
35	199.5	14.7	277	1	RIP4.SAPOR
36	199.5	14.7	277	1	RIP4.SAPOR
37	199.5	14.7	277	1	RIP4.SAPOR
38	199.5	14.7	277	1	RIP4.SAPOR
39	199.5	14.7	277	1	RIP4.SAPOR
40	199.5	14.7	277	1	RIP4.SAPOR
41	199.5	14.7	277	1	RIP4.SAPOR
42	199.5	14.7	277	1	RIP4.SAPOR
43	199.5	14.7	277	1	RIP4.SAPOR
44	199.5	14.7	277	1	RIP4.SAPOR
45	199.5	14.7	277	1	RIP4.SAPOR

34	119.5	8.8	319	1	SLTA_BP933
35	119	8.8	300	1	RIP3_MAIZE
36	112.5	8.3	280	1	RIP2_HORVU
37	111	8.2	343	1	YOC7_CAEFL
38	110	8.1	560	1	J160_HORVU
39	109.5	8.1	280	1	RIP1_HORVU
40	105.5	7.8	301	1	RIP9_MAIZE
41	103	7.6	304	1	RIP9_MAIZE
42	97.5	7.2	485	1	HKKA_YEAST
43	92.5	6.8	303	1	ALB3_MAIZE
44	92.5	6.8	484	1	YAG2_METJA
45	91	6.7	511	1	UDPG_DICDI

## ALIGNMENTS

RESULT 1	ID	RIP3.PHYAM	STANDARD:	PRT:	261 AA..
AC	P23339:				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DE	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Antiviral protein S (PAP-S) (Ribosome-inactivating protein) (rRNA				
DE	N-glycosidase) (EC 3.2.2.22).				
OS	Phytolacca americana (Common pokeweed) (Virginian pokeweed).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.				
OX	NCBI_TaxID=3527;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Seed;				
RX	MEDLINE=91242096; PubMed=1368643;				
RA	Kung S.-S., Kimura M., Funatsu G.;				
RT	"The complete amino acid sequence of the antiviral protein from the seeds				
RT	of pokeweed (Phytolacca americana).";				
RL	Agric. Biol. Chem. 54:3301-3318(1990).				
CC	- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN				
CC	SYNTHESIS IN VITRO.				
CC	- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one				
CC	specific adenosine on the 28S rRNA.				
CC	- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.				
CC	TYPE 1 RIP SUBFAMILY.				
CC	PIR: J0401; J0401.				
DR	HSSP: 003464; IAPA.				
DR	InterPro: IPR001574; RIP.				
DR	PIFAM: PFO0161; RIP. 1.				
DR	PRINTS: PR00396; SHIGARICIN.				
DR	PROSITE: PS00275; SHIGA.RICIN. 1.				
KW	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;				
KW	Toxin.				
FT	ACT_SITE 175 175 BY SIMILARITY.				
FT	DISULFID 34 258				
FT	DISULFID 84 105				
SO	SEQUENCE 261 AA; 29200 MW; D88B99962FE8399D CRC64;				
Query Match	80.8%; Score 1096.5; DB 1; Length 261;				
Best Local Similarity	82.8%; Pred. No. 2.8e-83;				
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;					
OY	2 INTTFDAGNATINKYATFMESLRNQAOKPKIKCYGIPMLPPTNTSPKLYLVKIQGNLK 61				
DB	1 INTTFDAGNATINKYATFMESLRNQAOKPKIKCYGIPMLPPTNTSPKLYLVKIQGNLK 60				
OY	62 TTTLMLRNRLNVYMGSDPFNGNKKRYHFNDFSTERTDVNTLSSSSSVAMSYNN 121				
DB	61 TTTLMLRNRLNVYMGSDPYD NKCRYHFNDFIKGTESVDVENTIKCPSSNPRVAKPTINN 119				
OY	122 SLVPTMEKKAEEVNSRNOVLQIOLISSDGKISGVDFPVKTEAFLLVAIQVSEAFNF 181				
DB	120 GLVPTLEKKAGVTSRNEVQLGIOLISSDGKISGVDFPVKTEAFLLVAIQVSEAFNF 179				

OY 182 KYIENOVKTNNFAYDDPVYINIEEKWKISAIHNKAGALPKPELYDAKTKMIVL 241  
 DB 180 KYIENOVKTNNFEDSPNDKVLDEENMGKISTAIHNSKNALPKPELKNADCTKMIVL 239  
 OY 242 RVDEINRDVALKRVNCTCQT 263  
 DB 240 RVDEIKPDVGLNLNVNCTCAT 261

RESULT 2  
 RIPL-PHYAM STANDARD: PRT: 313 AA.  
 ID RIPL-PHYAM STANDARD: PRT: 313 AA.  
 AC P10297;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Antiviral protein I precursor (PAP-I) (PAP-C) (Ribosome-inactivating  
 DE protein) (tRNA N-glycosidase) (EC 3.2.2.22).  
 GN PAPI.  
 OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllales: Phytolacaceae: Phytolacca.  
 OX NCBI\_TaxID=3527;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-62.  
 RC TISSUE-Leaf:  
 RX MEDLINE=92003676; Pubmed=1912488:  
 RA Lin Q., Chen Z.C., Antoniw J.F., White R.F.;  
 RT "Isolation and characterization of a cDNA clone encoding the  
 RL anti-viral protein from Phytolacca americana";  
 RN Plant Mol. Biol. 17:609-614(1991).  
 RN [2]  
 RP SEQUENCE OF 23-65.  
 RX MEDLINE=89193489; Pubmed=2930487;  
 RA Barbieri L., Bolognesi A., Cennini P., Falasca A.I., Minghetti A.,  
 RA Gaetano L., Guicciardi A., Lepini D., Miller S.P.;  
 RT "Ribosome-inactivating proteins from plant cells in culture";  
 RL Biochem. J. 257:801-807(1989).  
 RN [3]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Leaf:  
 RX MEDLINE=83290867; Pubmed=6885760:  
 RA Houston L.L., Ramakrishnan S., Hermodson M.A.;  
 RT "Seasonal variations in different forms of pokeweed antiviral protein,  
 RT a potent inactivator of ribosomes";  
 RL J. Biol. Chem. 258:9601-9604(1983).  
 RN [4]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Leaf:  
 RX MEDLINE=85023392; Pubmed=6091760;  
 RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;  
 RT "Characterization of translational inhibitors from Phytolacca  
 RT americana: amino-terminal sequence determination and antibody-  
 RL inhibitor conjugates";  
 RL Biochim. Biophys. Acta 790:154-163(1984).  
 RN [5]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Root:  
 RX MEDLINE=91064383; Pubmed=2248976;  
 RA Bolognesi A., Barbieri L., Abbondanza A., Falasca A.I., Carnicelli D.,  
 RA Battelli M.G., Stipe F.;  
 RT "Purification and properties of new ribosome-inactivating proteins  
 RT with RNA N-glycosidase activity";  
 RL Biochim. Biophys. Acta 1087:293-302(1990).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=94016586; Pubmed=8411176;  
 RA Monzingo A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D.;  
 RT "The 2.5 A structure of pokeweed antiviral protein";  
 RL J. Mol. Biol. 233:705-715(1993).  
 RN [7]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-284.  
 RX MEDLINE=99421320; Pubmed=10493577;  
 RA Kurinov I.V., Myers D.E., Irvin J.D., Uckun F.M.;  
 RT "X-ray crystallographic analysis of the structural basis for the  
 RT interactions of pokeweed antiviral protein with its active site  
 RL inhibitor and ribosomal RNA substrate analogs";  
 CC Protein Sci. 8:1765-1772(1999).  
 CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN  
 CC SYNTHESIS IN VITRO.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- TISSUE SPECIFICITY: SPRING LEAVES AND ROOTS.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X55383; CAA39054.1;  
 CC PIR: S02792; S02792.  
 CC PIR: S13469; S13469.  
 CC PDB: 1PAF; 31-JAN-94.  
 CC PDB: 1PAC; 31-JAN-94.  
 CC PDB: 1QCI; 15-SEP-99.  
 CC PDB: 1QCG; 15-SEP-99.  
 CC PDB: 1QCF; 15-SEP-99.  
 CC InterPro: IPR001574; RIP.  
 CC Pfam: PF00161; RIP.  
 CC PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense: Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 285  
 FT PROPEP 286 313  
 FT ACT\_SITE 198 198  
 FT DISULFID 56 281  
 FT STRAND 107 128  
 FT STRAND 25 29  
 FT HELIX 35 49  
 FT STRAND 55 56  
 FT STRAND 57 58  
 FT TURN 59 61  
 FT STRAND 65 66  
 FT TURN 71 78  
 FT STRAND 79 81  
 FT HELIX 82 89  
 FT STRAND 90 93  
 FT STRAND 94 102  
 FT TURN 103 105  
 FT STRAND 106 112  
 FT TURN 113 114  
 FT TURN 117 117  
 FT HELIX 118 127  
 FT TURN 131 132  
 FT STRAND 134 136  
 FT STRAND 139 139  
 FT HELIX 145 152  
 FT TURN 153 153  
 FT TURN 157 158  
 FT STRAND 162 162  
 FT HELIX 164 174  
 FT HELIX 175 176  
 FT TURN 182 195  
 FT TURN 196 196  
 FT HELIX 197 201  
 FT HELIX 203 211  
 FT TURN 212 214

ANTIVIRAL PROTEIN I.  
 BY SIMILARITY.

FT STRAND 217 217  
 FT HELIX 221 239  
 FT STRAND 241 241  
 FT TURN 242 243  
 FT STRAND 244 252  
 FT TURN 254 255  
 FT STRAND 258 263  
 FT HELIX 264 270  
 FT STRAND 274 274  
 SQ SEQUENCE 313 AA: 35219 MW: 2C57B2861EBA57F5 CRC64:

Query Match 77.4%; Score 1050; DB 1; Length 313;  
 Best Local Similarity 76.3%; Pred. No. 2,4e-79;

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

Oy 2 INTTFDAGNATINRYATFPMESLRNOAKDPKLCYGPMLPPTNSPKYLVKLOCANLK 61  
 Db 23 VNTTIYVSGSTISKATFPLNDLRNKAQPSLKCGIPMLPNTNPKYLVLELOCSNKK 82  
 Oy 62 TTTLMLRRNNLYVMGYSDPFNGNKCRIHFNIDITSTERTDVENTLCCSSSSRYAMSINYN 121  
 Db 83 TTTLMLRRNNLYVMGYSDPFNGNKCRIHFNIDITSTERTDVENTLCCSSSSRYAMSINYN 142  
 Oy 122 SLPTMEKKAENSRNOVOLGIISSDGIKISGVDSFPVKTEAFPLVAIQVSEAFARF 181  
 Db 143 SRPTLESKAGVSRQVOLGIIIDSNIGKISGVMSFTEKTEAEFLVAIQVSEAFARF 202  
 Oy 182 KYTENOVKTENFRAPDPKVINLEKMGKISEATINAKGALPKPLELVDAKGTWIVL 241  
 Db 203 KYTENOVKTENFRAPDPKVINLEKMGKISEATINAKGALPKPLELVDAKGTWIVL 262  
 Oy 242 RVDEINRDYALKYVNGTCOTT 263  
 Db 263 RVDEIKRPDVALNTYVGGSCOTT 284

RESULT 3  
 ID RIPAM PHAM STANDARD; PRT; 294 AA.  
 AC 003464:  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Antiviral protein alpha precursor (Pap-alpha) (Ribosome-inactivating  
 protein) (rRNA-N-glycosidase) (EC 3.2.2.22).  
 OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.  
 OX NCBI\_Taxid=3527;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=seed, leaf, and root.  
 RX MEDLINE=9309240; PubMed=1281438;  
 RA Katoaka J., Habuka N., Masuta C., Miyano M., Koiwai A.;  
 RA Ago H., Katoaka J., Tsuge H., Hakuba N., Inagaki E., Noma M.,  
 RA Miyano M.;  
 RT "X-ray structure of a pokeweed antiviral protein, coded by a new  
 RT genomic clone, at 0.23-nm resolution. A model structure provides a  
 RT suitable electrostatic field for substrate binding.";  
 RL Eur. J. Biochem. 225:369-374(1994).  
 RL Plant Mol. Biol. 20:879-886(1992).  
 RL [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=95010127; PubMed=7925458;  
 RA Ago H., Katoaka J., Tsuge H., Hakuba N., Inagaki E., Noma M.,  
 RA Miyano M.;  
 RT "X-ray structure of a pokeweed antiviral protein, coded by a new  
 RT genomic clone, at 0.23-nm resolution. A model structure provides a  
 RT suitable electrostatic field for substrate binding.";  
 RL Eur. J. Biochem. 225:369-374(1994).  
 CC -i- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN  
 CC SYNTHESIS IN VITRO. HAS ALSO BEEN SHOWN TO INHIBIT THE  
 CC REPLICATION OF MAMMALIAN VIRUSES. THE PROTEIN MAY PROVIDE A  
 CC MEANS OF CELLULAR SUICIDE UPON INVASION BY A VIRUS.  
 CC -i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.

CC -i- SUBUNIT: MONOMER.  
 CC -i- SUBCELLULAR LOCATION: Cell wall.  
 CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

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DR EMBL: D10600; BAA01451.1; -  
 DR PIR: S28421; S28421.  
 DR PDB: 1APA; 3I-JAN-94.  
 DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP. 1.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;

KW Toxin; Signal; Cell wall; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 285  
 FT PROPEP 286 294  
 FT ACT\_SITE 199 199  
 FT DISULFID 58 282  
 FT DISULFID 108 130  
 FT STRAND 28 31  
 FT HELIX 32 34  
 FT HELIX 37 51  
 FT STRAND 57 58  
 FT TURN 59 60  
 FT STRAND 61 63  
 FT TURN 67 68  
 FT STRAND 73 79  
 FT TURN 81 82  
 FT STRAND 85 91  
 FT TURN 92 94  
 FT STRAND 97 104  
 FT TURN 105 106  
 FT STRAND 107 113  
 FT TURN 114 115  
 FT STRAND 119 129  
 FT STRAND 136 138  
 FT STRAND 141 141  
 FT STRAND 147 154  
 FT TURN 155 155  
 FT HELIX 158 160  
 FT STRAND 163 163  
 FT STRAND 165 175  
 FT TURN 176 177  
 FT HELIX 183 195  
 FT TURN 196 197  
 FT TURN 198 198  
 FT HELIX 202 202  
 FT TURN 204 212  
 FT TURN 213 215  
 FT STRAND 218 218  
 FT STRAND 222 240  
 FT STRAND 242 242  
 FT TURN 243 244  
 FT STRAND 245 253  
 FT TURN 255 256  
 FT STRAND 259 264  
 FT STRAND 265 271  
 FT HELIX 265 271  
 FT STRAND 275 275  
 SQ SEQUENCE 294 AA: 33069 MW: F2BC27724FA85596 CRC64:

Query Match 74.8%; Score 1014.5; DB 1; Length 294;  
 Best Local Similarity 76.8%; Pred. No. 1,9e-76;

Matches 202; Conservative 21; Mismatches 37; Indels 3; Gaps 3;

Oy 2 INTTFDAGNATINRYATFPMESLRNOAKDPKLCYGPMLPPTNSPKYLVKLOCANLK 61  
 Db 23 VNTTIYVSGSTISKATFPLNDLRNKAQPSLKCGIPMLPNTNPKYLVLELOCSNKK 82

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Db 25 INTTFDGNATINKYATFMKSIHQADPLTKCYGIMLPNTNLTPTKLVTLVTLDDSSLK 84
QY 62 TITLMLRRNNLYVMGYSDPFNGNKKCRHYIFNDIT-STERDVENTLCSSSSRVAMSIN 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 TITLMLKRNLYVMGYADTYNG-KCRHYIFKDISWTERNDVMTLCPNPSRVCKNIN 143
QY 121 NSLPTMEKKAVERNNOVOIGIOLSSDIGKISVDSPKTEFFLVLAIONVSEAR 180
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 DSSPALEKKGW-RPRSOVQIGIOLNSGIRKYGVSFTEKTEAEFLVAIONVSEAR 202
QY 181 FKYLENOYKTNFRAFYDPKVINLEEKMGKISEAIIHAKNGALPKPLEVDAKETK 240
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 FKYLENOYKTNFRAFYDPKVINLEEKMGKISEAIIHAKNGALPKPLEVDAKETK 262
QY 241 LRVDENRVALLVYNGTCQT 263
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 LRVDIEPDVGLLKYNGTCQT 285

RESULT 4
RIP2_PHYAM STANDARD: PRT: 310 AA.
ID RIP2_PHYAM STANDARD: PRT: 310 AA.
AC 040772:
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein 2 precursor (PAP-II) (Ribosome-inactivating protein)
DE (rRNA N-glycosidase) (EC 3.2.2.22).
GN PAP2 OR PAP1I.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=94307398; PubMed=8034016;
RT "Isolation and characterization of a cDNA clone encoding the pokeweed
RT antiviral protein II from Phytolacca americana and its expression in
RT E. coli."
RL FEBS Lett. 347:268-272(1994).
RN [2]
RP SEQUENCE OF 26-55.
RC TISSUE=Leaf;
RX MEDLINE=85023392; PubMed=6091760;
RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;
RT "Characterization of translational inhibitors from Phytolacca
RT americana. Amino-terminal sequence determination and antibody-
RT inhibitor conjugates."
RL Biochim. Biophys. Acta 790:154-163(1984).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. INHIBITS PROTEIN
CC SYNTHESIS IN BOTH PROKARYOTES AND EUKARYOTES.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LATE SUMMER LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PROGRESSIVELY WITH THE AGING OF THE
CC PLANT.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
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CC
CC EMBL: X78628; CA55342.1;
CC HSSP: Q03464; IAPA.
CC InterPro: IPR001574; RIP.

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DR Pfam: PF00161; RIP; 1.
DR PRINTS: PRO0396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN_1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW toxin; Signal.
FT SIGNAL 1 25
FT CHAIN 1 25
FT PROPEP 2 310
FT ACT_SITE 197 197 BY SIMILARITY.
FT DISULFID 57 284 BY SIMILARITY.
FT DISULFID 106 123 BY SIMILARITY.
SQ SEQUENCE 310 AA; 34694 MW; 4D3BB001D7259D9P CRC64;

Query Match 33.4%; Score 453; DB 1; Length 310;
Best Local Similarity 41.0%; Pred. No. 3.4e-30;
Matches 112; Conservative 41; Mismatches 94; Indels 26; Gaps 11;

QY 3 NTTFDGNATINKYATFMESLRNQADPKIKCYGIMLPNTNTPPYLLVLCAGANLKT 62
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 25 SNIVEDYENATPEYNSFLTSLREAVNDKRLTCHGMATTLTEOPKIVLVLDKFGS-CT 83
QY 63 ITLMLRRNNLYVMGYSDPFNGNKKCRHYIFNDITERTDVENTLCSSSSR--VAMSIN 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 FTLAIRKGNLTLEGSIDYNG-KCRHYIFKD-----SSDAQETVCPGDKSKPTGNINPY 138
QY 121 NSLPTMEKKAVERNNOVOIGIOLSSDIGKISVDSPF-----VKTEAFLVLAIONVS 176
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 EKSKTGESK--GARKRLGLGKITLSRMCKITYGKATDQKQYKNEAEFLVLAIONV 196
QY 177 EAARFKYLENOYKTNFRA--FYDPKVINLEEKMGKISEAIIHAKNG-----ALPKPE 229
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 197 EASFKYLENKVKAFPDANGYDPDAISLEKMDVSKEYI--AKYGTSGDSIVTLPGD 254
QY 230 LVDAKGRKIVYLRVDENRVDY-ALLKTVNGTCQ 261
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 LKDENNRPWTATATMNDLKNIMALLTHV--TK 285

RESULT 5
RIP6_SAPOF STANDARD: PRT: 299 AA.
ID RIP6_SAPOF STANDARD: PRT: 299 AA.
AC P20636; Q41392;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-6 precursor (SAP-6) (SO-6)
DE (rRNA N-glycosidase) (EC 3.2.2.22).
GN SAP6.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE OF 1-283 FROM N.A., AND SEQUENCE OF 25-115; 206-213 AND
RP 234-277.
RC TISSUE=Leaf;
RX MEDLINE=89338421; PubMed=2547612;
RA Benatti L., Saccardo M.B., Dani M., Nitli G., Sassano M.,
RA Lorenzetti R., Lappi D.A., Soria M.,
RT "Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-
RT inactivating protein from Saponaria officinalis."
RL Eur. J. Biochem. 183:465-470(1989).
RN [2]
RP SEQUENCE OF 25-277 FROM N.A.
RX MEDLINE=93203250; PubMed=8454624;
RA Bartelemy I., Martineau D., Ong M., Matsunami R., Ling N.,
RA Benatti L., Cavallaro U., Soria M., Lappi D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli."
RL Eur. J. Biol. Chem. 268:6541-6548(1993).
RN [3]
RP SEQUENCE OF 275-299 FROM N.A.

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[illegible]

```

QY      2 NITIFEDGNGNTINKYATPFMSLJPNQAKDKPLKCYGPM-LPPTNSTPKRYLLXKQGAU. 60
      : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      1 VTSITLIDLVTNTAQQYSSFYDKIRNNKYNLWGGDIAVICGPKPEKFLINPQSS- 59
      : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY      61 KTIITMLERNNLVYMGVSDPENGKCR-YHIFNDITSTERTDVENTLKSSSSRYAMSI 119
      : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db      60 GVSISGLTKRDLVLYAVATLMDNTVNRAYVFRSEITSALT----ALPEATVANOQKALE 115
      : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY      120 YMSLPTMKERAAEV-----NSRNQVQLQIQLSSDICKISGVDSFPKTKTAFLVLAIOV 175
      : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

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CC				use by non-profit institutions as long as its content is in no way
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CC				entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announcement/</a>
CC				<a href="http://www.isb-sib.ch/announcement/">or send an email to license@isb-sib.ch</a> ).
DR	EMBL:	X5925;	CAA41948.1;	-
DR	EMBL:	X69132;	CAA48886.1;	-
DR	EMBL:	X69133;	CAA48887.1;	-
DR	PIR:	S17933;	RLOHG2.	
DR	HSSP:	P10297;	IOCG.	
DR	Interpro:	IPRO01574;	RIP.	
DR	pfam:	PF00161;	RIP.	
DR	PRINTS:	PR00396;	SHGARICIN.	
DR	PROSITE:	PS00275;	SHIGA_RICIN.1.	
KW	Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; signal;			
KW	Multigene family.			
KW	SIGNAL	1	24	
FT	CHAIN	25	292	RIOSOME-INACTIVATING PROTEIN SAKORIN-2.
FT	AC1_SITE	200	200	BY SIMILARITY.
FT	VARIANT	72	72	D -> E.

```

RESULT 9
RIP0_DIACA ID RIP0_DIACA STANDARD: PRT: 293 AA.
AC P24476;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein DAP-30 precursor (Ribosome-inactivating protein)
OS Dianthus carophyllus (Carnation) (Clove pink).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Dianthus.
OX NCBI_Taxid=3570;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91355219; PubMed=1840496;
RA Legname G., Bellosta P., Gromo G., Modena D., Keen J.N., Roberts L.M.,
RA Lord J.M.;
RT "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome
RT inactivating protein from Dianthus carophyllus.";
RL Biochim. Biophys. Acta 1090:119-122(1991).
RN [2]
RP SEQUENCE OF 24-82.
RC TISSUE=leaf;
RX MEDLINE=92037998; PubMed=1936243;
RA Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P.,
RA Huang H.I., Chen H.-C.;
RT "A new class of anti-HIV agents: GAP31, DAPs 30 and 32.";
RL FEBS Lett. 291:139-144(1991).
CC -I- FUNCTION: SINGLE-CHAIN RIBOSOME-INACTIVATING PROTEIN, POSSESSING
CC HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
CC AND TO INACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INJECTION AND
CC REPLICATION.
CC -I- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
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[illegible]

RA Hosur M.V., Nair B., Satyamurthy P., Misquith S., Suroolia A.,  
 RA Kannan K.K.;  
 RT "X-ray structure of gelonin at 1.8-A resolution.";   
 RL J. Mol. Biol. 250:368-380(1995);  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC -----  
 DR EMBL: L12243; AAI6312.1;  
 DR PIR: S16489; S16489.  
 DR HSSP: P09889; 1MRJ.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP.1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA-RICIN; FALSE\_NEG.  
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
 KW Glycoprotein.  
 FT SIGNAL 1 26  
 FT PROPEP 27 46 POTENTIAL.  
 FT CHAIN 47 237 RIBOSOME-INACTIVATING PROTEIN GELONIN.  
 FT PROPEP 298 316 MISSING IN MATURE PROTEIN.  
 FT DISULFID 90 96  
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .).  
 FT ACT\_SITE 212 212  
 FT CONFLICT 90 90 C -> K (IN REF. 2).  
 FT CONFLICT 93 93 P -> D (IN REF. 2).  
 SQ SEQUENCE 316 AA: 35418 MW: 1252FE3E710901B85 CRC64:  
 Query Match 23.1%; Score 313; DB 1; Length 316;  
 Best Local Similarity 32.1%; Pred No. 1.2e-18;  
 Matches 86; Conservative 50; Mismatches 110; Indels 22; Gaps 8;  
 QY 2 INTTFDAGNATINKYATFMESLRNQADPKLKCXGIMLPDPTNTPK--YLVKLOGAN 59  
 DB 48 LDTVSFSTKATYTYVNPDLRYKLK-PGNSNGIPLLRKCDPKCFYVALSDNN 106  
 QY 60 LKTIPLMRNNLLYMGYSDDPNKCKRHIFNDITSTERTDV-ENTLCSSSSSRVAMSI 118  
 DB 107 GOLAEIADVTSVYVGYO---VRNRSYFFKADPAAYEGLFKNT-----IKTRL 153  
 QY 119 NNSLYPTMEKKAENVSRNOYOLGLOISDGIK--SGVDSFPVKTEAFILVAIQWVS 176  
 DB 154 HGGGYSFSLF--GEAYRETTDLGLEPIRLIGIKKIDENAIDWKYDETIASSLLVYQWS 211  
 QY 177 EAARPKYIENOVKTNFRAFYPPDKVINLEEKMGKISEAIIH-NAKNGALPKPLELVDAKG 235  
 DB 212 EAARPTFIENQRRNFPQRIIPRANNTISLEKNKMGKLSLOITSGANGFSEAVELERANG 271  
 QY 236 TKMYLVRLDEINRDVALLKYNGCQTT 263  
 DB 272 KKYVTAVDOVKPKIALLKPVDKDKPTS 299

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:  
 OC eucosids: Malpighiales: Euphorbiaceae: Ricinus.  
 OX NCBI\_TaxID=3988;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86067214; PubMed=2999712;  
 RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,  
 RA Weaver R.F.;  
 RT "Genomic cloning and characterization of a ricin gene from Ricinus  
 RT communis.";  
 RL Nucleic Acids Res. 13:8019-8033(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92163016; PubMed=1371405;  
 RA Tregear J.W., Roberts L.M.;  
 RT "The lectin gene family of Ricinus communis: cloning of a functional  
 RT ricin gene and three lectin pseudogenes.";  
 RL Plant Mol. Biol. 18:515-525(1992).  
 RN [3]  
 RP SEQUENCE OF 12-576 FROM N.A.  
 RX MEDLINE=85179479; PubMed=3838723;  
 RA Lamb A., Roberts L.M., Lord J.M.;  
 RT "Nucleotide sequence of cloned cDNA coding for preproricin.";  
 RL Eur. J. Biochem. 148:265-270(1985).  
 RN [4]  
 RP SEQUENCE OF 36-302.  
 RA Yoshitake S., Funatsu G., Funatsu M.;  
 RT "Isolation and sequences of peptic peptides, and the complete  
 RT sequence of the chain of ricin-D.";  
 RL Agric. Biol. Chem. 42:1267-1274(1978).  
 RN [5]  
 RP SEQUENCE OF 315-576.  
 RA Funatsu G., Kimura M., Funatsu M.;  
 RT "Primary structure of Ala chain of ricin D.";  
 RL Agric. Biol. Chem. 43:2221-2224(1979).  
 RN [6]  
 RP CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.  
 RX MEDLINE=90344223; PubMed=1368517;  
 RA Kimura Y., Kusunoku H., Tada M., Takagi S., Funatsu G.;  
 RT "Structural analyses of sugar chains from ricin A-chain variant.";  
 RL Agric. Biol. Chem. 54:157-162(1990).  
 RN [7]  
 RP REVIEW  
 RX MEDLINE=21480122; PubMed=11595634;  
 RA Olsnes S., Kozlov J.V.;  
 RT "Ricin.";  
 RL Toxicon 39:1723-1728(2001).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RX MEDLINE=87165983; PubMed=3558397;  
 RA Monfort W., Villafraza J.E., Monzinger A.F., Ernst S.R., Katzin B.,  
 RA Rutenber E., Xuong N.H., Hamlin R., Roberts J.D.;  
 RT "The three-dimensional structure of ricin at 2.8 A.";  
 RL J. Biol. Chem. 262:5398-5403(1987).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=91352004; PubMed=1881881;  
 RA Katzin B.J., Collins E.J., Roberts J.D.;  
 RT "Structure of ricin A-chain at 2.5 A.";  
 RL Proteins 10:251-259(1991).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
 RX MEDLINE=91352005; PubMed=1881882;  
 RA Rutenber E., Roberts J.D.;  
 RT "Structure of ricin B-chain at 2.5-A resolution.";  
 RL Proteins 10:260-269(1991).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE=95082010; PubMed=790130;  
 RA Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,  
 RA Pauptit R.A.;  
 RT "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";

RL J. Mol. Biol. 244:410-422(1994).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.  
 RX MEDLINE:96374222; PubMed:8780513;  
 RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,  
 RA Molina-Svith M.C., Robertus J.D.;  
 RT "Structure and activity of an active site substitution of ricin A  
 RT chain."  
 RL Biochemistry 35:11098-11103(1996).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
 RX MEDLINE:97240820; PubMed:9086280;  
 RA Yan X., Hollis T., Svith M., Day P., Monzingo A.F., Milne G.W.,  
 RA Robertus J.D.;  
 RT "Structure-based identification of a ricin inhibitor."  
 RL J. Mol. Biol. 266:1043-1049(1997).  
 RN [14]  
 RP MUTAGENESIS.  
 RX MEDLINE:93165612; PubMed:1287657;  
 RA Kin Y., Robertus J.D.;  
 RT "Analysis of several key active site residues of ricin A chain by  
 RT mutagenesis and X-ray crystallography."  
 RL Protein Eng. 5:775-779(1992).  
 CC -1- FUNCTION: Ricin is highly toxic to animal cells and to a less  
 CC extent to plant cells. The A chain is responsible for inhibiting  
 CC protein synthesis through the catalytic inactivation of 60S  
 CC ribosomal subunits. It acts as a glycosidase that removes a  
 CC specific adenine residue from an exposed loop of 28S ribosomal  
 CC RNA. As this loop is involved in the binding of elongation  
 CC factors, the modified ribosomes are unable to support ribosome  
 CC synthesis. The A chain can inactivate a few thousand ribosomes  
 CC per minute, thus inactivating them faster than the cell can make  
 CC new ones. A single A-chain molecule can therefore kill an animal  
 CC cell. The B chain binds to cell receptors and facilitates the  
 CC entry into the cell of the A chain. B chains are also responsible  
 CC for cell agglutination (lectin activity). It binds to beta-D-  
 CC galactopyranoside moieties.  
 CC CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC -1- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 271.  
 CC MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.  
 CC CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS  
 CC WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).  
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 CC -----  
 CC EMBL: X01179; CAA26939.1; -  
 DR EMBL: X52908; CAA37095.1; -  
 DR EMBL: X02388; CAA26230.1; -  
 DR EMBL: A12892; CAA01058.1; -  
 DR PIR: A24041; RLCSD.  
 DR PDB: 2AAT; 31-JAN-94.  
 DR PDB: 1AP6; 31-JAN-94.  
 DR PDB: 1FMP; 31-OCT-93.  
 DR PDB: 1IFS; 14-JAN-98.  
 DR PDB: 1IFU; 14-JAN-98.  
 DR PDB: 1IRC; 31-OCT-93.  
 DR PDB: 1OBS; 16-JUN-97.  
 DR PDB: 1OBT; 16-JUN-97.  
 DR PDB: 1BR5; 02-SEP-98.

DR PDB: 1BR6; 02-SEP-98.  
 DR GLYCOSITEDB: P02879; -  
 DR InterPro: IPR001574; RIP.  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR Pfam: PF00161; RIP; 1.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR SMART: SM00458; RICIN; 2.  
 DR PROSITE: PS50231; RICIN\_B\_LLECTIN; 2.  
 DR PROSITE: PS00275; SHIGA; RICIN; 1.  
 DR Plant defense: Hydrolase: Protein synthesis inhibitor: Toxin; Repeat;  
 KW Glycoprotein; Lectin; Signal; 3D-structure.  
 FT SIGNAL 1 35  
 FT CHAIN 36 302  
 FT PEPTIDE 303 314  
 FT CHAIN 315 576  
 FT DOMAIN 321 448  
 FT DOMAIN 451 575  
 FT REPEAT 331 373  
 FT REPEAT 374 414  
 FT REPEAT 417 449  
 FT REPEAT 462 497  
 FT REPEAT 501 540  
 FT REPEAT 543 570  
 FT ACT\_SITE 212 212  
 FT DISULFID 294 318  
 FT DISULFID 334 353  
 FT DISULFID 377 394  
 FT DISULFID 465 478  
 FT DISULFID 504 521  
 FT CARBOHYD 45 45  
 FT CARBOHYD 271 271  
 FT CARBOHYD 409 409  
 FT CARBOHYD 449 449  
 FT CONFLICT 76 76  
 FT CONFLICT 551 551  
 FT STRAND 43 47  
 FT STRAND 49 50  
 FT TURN 50 50  
 FT HELIX 53 67  
 FT STRAND 73 74  
 FT TURN 75 76  
 FT STRAND 77 79  
 FT TURN 88 90  
 Query Match 21.4%; Score 291; DB 1; Length 576;  
 Best Local Similarity 30.4%; Pred. No. 1; 7e-16;  
 Matches 83; Conservative 44; Mismatches 100; Indels 46; Gaps 10;  
 QY 5 ITFDAGNATINKATPMESLRNOAKDPKLCYGPMLPTNSTP---KYLVLQGANLK 61  
 DB 44 INTTGTGATVOSTNTNIRAVRGULTTGADVRHEIPVLPNRVGLPIORFLIVLSMAEL 103  
 QY 62 TITLMLRNNLVYMGYSDFPENGKCRY-----HIFNDITSTERPDVENTLCS 108  
 DB 104 SVTLALDVTNAVYVGR---AGNSAVFFHPDNOEDAEATHLF-----EDVON---- 148  
 QY 109 SSSSRVAMSINYSLSLPTMEKKAEVSRNOVOIGITLSSDICKI-----SCVDSRPVKTE 164  
 DB 149 ---RYTFAGGN--YDRLEQLAG-NLRENIELGNPLLEAISALVYSGTGTOIPTTLAR 201  
 QY 165 AFFLVAIOKVSSEARFKYLENOVKT--NFNRAFYDPKVINLEKKMGKISEAIIHNAKNG 222  
 DB 202 SF--IICIQMISAAFOYIEGEMRRIRIRNRSADPSVITLLENSGRSLTAIQESNCG 259  
 QY 223 ALKPPLDYDAKGTWIVLVEIDINRDVALKY 255  
 DB 260 AFASPIQLORRNGSKFSYDVSTLIIILALMV 292  
 RESULT 12

RIP1-TRIAN STANDARD: PRT: 294 AA.

AC P56626; 092077.

DT 15-DEC-1998 (Rel. 37, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Type I ribosome-inactivating protein trichosanguina precursor (rRNA N-glycosidase) (EC 3.2.2.22) (RIP) (trichosanguin).

GN TCA.

OS Trichosanthes anguina (Snake gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

OX NCBI\_TaxID=50544;

RN [1]

RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.

RC STRAIN=cv. Anguina; TISSUE=seed;

RX MEDLINE=99132006; PubMed=991318;

RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H., Lin J.-Y.;

RT "Purification, characterization and molecular cloning of trichosanguin, a novel type I ribosome-inactivating protein from the seeds of Trichosanthes anguina."

RT Biochem. J. 338:211-219(1999).

RL [2]

RN SEQUENCE OF 20-264.

RC TISSUE=Seed;

RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;

RT "Amino acid sequence of trichosanguina, a ribosomal-inactivating protein from Trichosanthes anguina seeds."

RT J. Biomed. Sci. 3:178-186(1996).

CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN RIBOSOMES.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUBFAMILY.

CC -----

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CC -----

CC EMBL: AF055086; AAD02686.1; -

CC DR HSSP: P33185; 1BRV.

CC DR InterPro: IPR001574; RIP.

CC DR Pfam: PF00161; RIP.1.

CC DR PRINTS: PRO00396; SHIGARICIN.

CC DR PROSITE: PS00275; SHIGA\_RICIN; FALSE\_NEG.

CC KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;

CC KW Glycoprotein; Signal.

CC FT SIGNAL 1 19

CC FT CHAIN 20 264

CC FT TYPE I RIBOSOME-INACTIVATING PROTEIN

CC FT TRICHOANGUINA.

CC FT PROPEP 265 294

CC FT ACT\_SITE 177 177

CC FT ACT\_SITE 180 180

CC FT CARBOHYD 70 70

CC FT CARBOHYD 220 220

CC FT CONFLICT 51 51

CC FT CONFLICT 65 65

CC FT CONFLICT 84 84

CC FT CONFLICT 152 152

CC FT CONFLICT 174 174

CC FT CONFLICT 245 245

CC FT SEQUENCE 294 AA; 32234 MW; DA4FB7CE3290994 CRC64;

Query Match 21.2%; Score 287.5; DB 1; Length 294;  
Best Local Similarity 30.7%; Pred. No. 1,3e-16;  
Matches 80; Conservative 52; Mismatches 104; Indels 25; Gaps 9;

QY 2 INTTFDAGNATINKYATFMEESLRQADPKIKCYGIPMLPPTNSTPKYL-LVKIGAGNL 60

DB 18 IDVSFDDSTAKKSYSSFTQLRALPQTGTCV-GIDPLPSTAGSOMFRFFNLTVND 76

QY 61 KTTTLRLRRNLVYGVY-SDPENGKCKRHHFNDITSRTERTVENTLSSSSSRAMSTN 119

DB 77 ETVTVAVNTVNTVYIAYRADAVS-----YFFED---TPAEAFKIFAGTKVKLPYSGN 127

QY 120 YNSLYPTEKKAQVNSRNQVGLG10LSSD1GKISGVDSFPKYTEAFPLIYAIQVSEAA 179

DB 128 YDKLOSIVGKQ-----RMIEIGIPALSS---A1TNMYVYDYQSTAAALLVLIQCTAEEA 179

QY 180 RFKYIENGVKTNFNRAFYDPDPKVITLLEKMKGISALINAK---NGALPKPLEYDANKT 236

DB 160 RKXYLEQOVSSHISNFPYQNAVISLENKMGALSKQ10IANTRTGHPENVEYLVNPDCT 239

QY 237 KWIYLRVDE--INRDVALKY 255

DB 240 RESVNTSAGVYKGNIKLLY 260

RESULT 13

RIP3\_SAPOF

ID RIP3\_SAPOF STANDARD: PRT: 236 AA.

AC P27560;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein saporin-3 (SAP-3) (SO-3) (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).

GN SAP3.

OS Saponaria officinalis (Common soapwort).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Saponaria.

OX NCBI\_TaxID=3572;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=92049247; PubMed=1719367;

RA Fordham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;

RT "Characterisation of saporin genes: in vitro expression and ribosome inactivation."

RT Mol. Gen. Genet. 229:460-466(1991).

CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR PHARMACOLOGICAL APPLICATIONS.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

CC TYPE 1 RIP SUBFAMILY.

CC -----

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CC -----

CC EMBL: X59256; CAA41949.1; -

CC DR PIR: S17932; S17932.

CC DR HSSP: P10297; 10CG.

CC DR InterPro: IPR001574; RIP.

CC DR Pfam: PF00161; RIP.1.

CC DR PROSITE: PS00275; SHIGA\_RICIN; 1.

CC KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;

CC KW Multigene family.

CC FT NON\_TER 1 1

CC FT ACT\_SITE 148 148

CC FT SEQUENCE 236 AA; 26591 MW; DE3D68BA50FCCE054 CRC64;

Query Match 20.9%; Score 283; DB 1; Length 236;

Best Local Similarity 35.8%; Pred. No. 2.4e-16;  
Matches 86; Conservative 41; Mismatches 87; Indels 26; Gaps 10;

QY 30 DKRLCYGIPM-LPTDNTSPKYLKLGQANLKTITLWLRNNLYVMGSDPFNGKCR- 87  
DB 1 DNLKLYGGTDIVICPPSRDKFLRLPFOSSR-GTVSLGKRENLVAVLAMDANVNA 59  
QY 88 YHIFDITSTERTDVENTLCCSSSSSVAMSYNSLYPTMEKRAEV---NSRNOVOLGI 143  
DB 60 YFEGEITISALTE---TLPEATYANQKALEYEDYOSIEKNKTEGDKTRKELGLOI 115  
QY 144 QILSS---DIGKISGVDPVTEAFELLVAIQWSEARFYENQVKTNFNRAFPDP 200  
DB 116 NLSTLMDAVNKKARV---VKNEARFLIAIQMTAEARFRYIQNLVTKNPNKFNSED 171  
QY 201 KYINLEEKWKISEAH-NAKNGALPKPELVDACTKIVLRVDEINDVALLKYVNT 259  
DB 172 KVIQFOVNSKISKALYGDANKGVFNKDYDFGFGK---VRQVKDL-QMGLMLVLTGT 224

RESULT 14  
AGCL\_RICCO STANDARD: PRT: 564 AA.  
ID AGCL\_RICCO STANDARD: PRT: 564 AA.  
AC P06750;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Agglutinin precursor (RCM) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].  
OS Ricinus communis (Castor bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
OX NCBI\_TaxID=3988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86059449; PubMed=2999130;  
RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;  
RT "The primary sequence of Ricinus communis agglutinin. Comparison with ricin."  
RL J. Biol. Chem. 260:15682-15686(1985).  
RN [2]  
RP SEQUENCE OF 303-564.  
RC TISSUE-Seed:  
RA Araki T., Yoshioke Y., Funatsu G.;  
RT "The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."  
RL Biochim. Biophys. Acta 872:277-285(1986).  
RN [3]  
RP SEQUENCE OF 303-337.  
RX MEDLINE=80178723; PubMed=6768555;  
RA Lin T.T.-S., Li S.S.-L.;  
RT "Purification and physicochemical properties of ricins and agglutinins from Ricinus communis."  
RL Eur. J. Biochem. 105:453-459(1980).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.  
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CC -----  
DR EMBL: M12089; AAA33869.1;  
DR EMBL: S40368; AAB22584.1;  
DR PIR: A24261; RLCSAG.  
DR HSSP: P02879; 1BR6.

DR GlycosylatedDB: P06750; -.  
DR InterPro: IPR001574; RIP.  
DR InterPro: IPR000772; Ricin\_B\_lectin.  
DR Pfam: PF00161; RIP: 1.  
DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
DR PRINTS: PR00396; SHIGARICIN.  
DR SMART: SM00458; RICIN: 2.  
DR PROSITE: PS50231; RICIN\_B\_LECTIN; 2.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
KW Plant defense; Hydrolase; protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 290  
FT PROPEP 291 302  
FT CHAIN 303 564  
FT DOMAIN 309 436  
FT DOMAIN 439 563  
FT REPEAT 319 361  
FT REPEAT 362 402  
FT REPEAT 405 437  
FT REPEAT 450 485  
FT REPEAT 489 528  
FT REPEAT 531 558  
FT ACT\_SITE 200 200  
FT DISULFID 282 306  
FT DISULFID 322 341  
FT DISULFID 355 382  
FT DISULFID 453 466  
FT DISULFID 482 509  
FT CARBOHYD 34 34  
FT CARBOHYD 259 259  
FT CARBOHYD 397 397  
FT CARBOHYD 437 437  
FT CONFLICT 331 331  
FT CONFLICT 362 362  
FT CONFLICT 374 374  
FT CONFLICT 404 404  
FT CONFLICT 552 552  
SQ SEQUENCE 564 AA: 62851 MW: D455FA2A72F609759 CRC64;

Query Match 20.0%; Score 271.5; DB 1; Length 564;  
Best Local Similarity 28.7%; Pred. No. 6.6e-15;  
Matches 77; Conservative 47; Mismatches 107; Indels 37; Gaps 7;

QY 5 IFPDAGNATINKYAFPMESLRNQADPKKCGIPLPTDNTSP---KYLKLGQANLX 61  
DB 33 INFTTADATVESYTNFIRAVRSHLTGTGADVRHEIPVLRVGLPLISQRTLVLSNHAEL 92  
QY 62 TITLMLRRNNLYVMG-----YSDPFNGKCRHIFNDITSTERTDVENTLCCSSS 111  
DB 93 SVTLALDVTNNAVYVCGRAGNSAVFFHPDQDEAEATHLF-----TDVON----- 137  
QY 112 SVAMSYNSLYPTMEKRAEVNSRNOVOLGIQLSSDIGKI--SCVDSFPVKTAEFFIL 169  
DB 138 ---SFTFAFGVNDRLQGLGCL--RENIELGLPLEDAISALYYVSTGTOIPFLARSPM 192  
QY 170 VALQWSEARFYENQVKT--NFRARVPPKYINLEEKWKISEAHNNKNGALRPP 227  
DB 193 VCIQWSEARFYENQVKT--NFRARVPPKYINLEEKWKISEAHNNKNGALRPP 227  
QY 228 LELVDAGTKWIVLRVDEINRDVALLKY 255  
DB 253 IQLQRNGSKFNVYDSILIPILALMVY 280

RESULT 15  
RIP2\_BRYDI STANDARD: PRT: 282 AA.  
ID RIP2\_BRYDI STANDARD: PRT: 282 AA.  
AC P98184; O9S8J0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein bryodin II precursor (rRNA N-

DB 250 NVNSPVVKGIALLLY 264

Search completed: July 2, 2003, 11:37:37  
Job time: 12.338 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 19.022 Seconds

(without alignments)  
1329.163 Million cell updates/sec

Title: US-09-978-274A-4

Sequence: 1 MUNITFDAGNATINKYATF.....DEINRDVALLKYVNGTCQTT 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096.5	80.8	261	2 JF0401	antiviral protein
2	1050	77.4	313	2 S17757	RNA N-glycosidase
3	1014.5	74.8	294	2 S28421	RNA N-glycosidase
4	453	33.4	310	2 S46239	ribosome-inactivat
5	425.5	31.4	289	2 T12573	RNA N-glycosidase
6	394	29.0	272	2 JCA811	betavulgin - beet
7	343.5	25.3	253	2 A58923	RNA N-glycosidase
8	342	25.2	283	2 S05205	RNA N-glycosidase
9	341	25.1	253	2 S29931	RNA N-glycosidase
10	337	24.8	253	2 S28539	RNA N-glycosidase
11	336	24.8	253	2 S28542	RNA N-glycosidase
12	335.5	24.7	292	1 R10H2	RNA N-glycosidase
13	335	24.7	293	2 S28541	RNA N-glycosidase
14	319.5	23.5	293	2 S17519	RNA N-glycosidase
15	313	23.1	316	2 J70753	RNA N-glycosidase
16	291	21.4	576	1 R1CSD	ricin D precursor
17	288.5	21.3	245	2 JCA840	RNA N-glycosidase
18	283	20.9	236	2 S17932	RNA N-glycosidase
19	271.5	20.0	564	1 R1CSAC	agglutinin precurs
20	267	18.9	278	2 A39817	RNA N-glycosidase
21	247.5	18.2	286	1 RLPUGG	RNA N-glycosidase
22	243	17.9	278	2 S23519	beta-luifin - smoo
23	241	17.8	247	2 J00393	karasurin - Mongol
24	241	17.8	289	1 R1RZT	RNA N-glycosidase
25	240	17.4	247	2 JCS032	karasurin-B - Tric
26	236	17.0	250	2 J2LSA	abrin-a precursor
27	230.5	17.3	528	1 T2LSA	abrin-b precursor
28	229	16.9	527	2 S32430	

30	217.5	16.0	251	2 C39761	abrin (clone 7.2)
31	215	15.8	286	2 S25560	RNA N-glycosidase
32	211	15.5	286	2 JC4235	RNA N-glycosidase
33	209.5	15.4	528	2 S32431	abrin-d precursor
34	209.5	15.4	562	2 S16022	abrin-c precursor
35	200	14.7	254	2 PD0018	mistletoe lectin I
36	199.5	14.7	277	2 S22494	RNA N-glycosidase
37	198	14.6	570	2 S62627	agglutinin I precu
38	165.5	12.2	157	2 S17934	RNA N-glycosidase
39	148	10.9	106	2 R39761	abrin (clone 3.7)
40	131	9.7	32	2 S38528	RNA N-glycosidase
41	124.5	9.2	319	2 S15695	shiga-like toxin I
42	124	9.1	315	1 XUBPH9	Shiga-like toxin C
43	124	9.1	315	2 A53887	Shiga-like toxin I
44	121.5	9.0	319	2 I60446	Shiga-like cytotox
45	121	8.9	315	1 A28626	Shigella toxin cha

#### ALIGNMENTS

##### RESULT 1

JF0401

C:Species: Phytolacca americana (Virginian pokeweed)

C>Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 07-May-1999

C:Accession: JF0401

R:Kung, S.S.; Kimura, M.; Funatsu, G.

Agric. Biol. Chem. 54, 3301-3318, 1990

A:Title: The complete amino acid sequence of antiviral protein from the seeds of pk

A:Reference number: JF0401; MUID:91242096; PMID:1368643

A:Accession: JF0401

A:Molecule type: protein

A:Residues: 1-261 <KUN>

A:Experimental source: seed

C:Comment: This protein prevents the replication of a number of plant viruses, and

C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology

C:Keywords: disulfide bond; glycoprotein

F:6-254/Domains: RNA N-glycosidase homology <RNG>

F:10,44,255/Binding site: carbohydrate (Asn) (covariant) #status experimental

F:34-258,84-105/Disulfide bonds: #status experimental

Query Match 80.8%; Score 1096.5; DB 2; Length 261;

Best Local Similarity 82.8%; Pred. No. 2.8e-81;

Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY	2	INTTFDAGNATINKYATFPMESLRNOADPKLCYGPMLPDTNSTPYLLVKIAGANIK 61
DB	1	INTTFDAGNATINKYATFPMESLRNEADPKLCYGPMLPDTNSTPYLLVKIAGANIK 60
QY	62	TTTLMRLNNLVYMGSDPFGNCKRHYHFNDFSTERTDVNTLCSSSSSVAMSIYN 121
DB	61	TTTLMRLNNLVYMGSDPFGNCKRHYHFNDFSTERTDVNTLCSSSSSVAMSIYN 119
QY	122	SLYPTMEKKAENVSNNOVGLGILSDIGKISGVDPVKTEAFELLVATIQWSEAAIK 181
DB	120	GLYPTLEKKAGVTSNENVOGLGILSDIGKISGVDPVKTEAFELLVATIQWSEAAIK 179
QY	182	KYIENQVKTNFRAFYDPKVIINLEEKWKCISEAIHNAKNGALPKPLEIYDAKGYKWIIVL 241
DB	180	KYIENQVKTNFRAFYDPKVIINLEEKWKCISEAIHNAKNGALPKPLEIYDAKGYKWIIVL 239
QY	242	RVDENRDVALLKYVNGTCQTT 263
DB	240	RVDENRDVALLKYVNGTCQAT 261

##### RESULT 2

S17757

RNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed

N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosor

C:Species: Phytolacca americana (Virginian pokeweed)

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999



Db 26 VFEDLETASKTKGFTLSLNRINIVDSKLVYEGIPMLPARIKPAVYLLAEELKAKKAGTDI 85

OY 61 KITTLMLRRNNLYVMGYSDPFNGNCKRHIFNDITSTERTDVENTLSCSSSRVAMSINY 120

Db 86 -TITLAVSKNDLTVVAFPTDQVAG-KLRAHYFPDITSLATAKAIFPT-----AVQYIQIGY 137

OY 121 NSLYPMMEKKAEVNSNOVLGIQLSDSIGKISG---VDSFPVTEAFELLVAIQWSE 177

Db 138 TSNVYIEGAGAGN-RVNFQLGFPVKIKEYMLVYGNVDSOYRSEARFLLAIAQWAE 196

OY 178 AARFKYIENOVKTNFNRAFYPPKVIINLEEKMGKISIAIHNAKNGALPKPLELVAIAKTR 237

Db 197 AARFKYVESALINN---VVPDYKVPSELENNMSKISEIGRAKVAKKVISPPIELVANSNGK 252

OY 238 WIYLRVDEINRDYALLKYV 256

Db 253 WTVNOVSDIKPDWGIILSYV 271

RESULT 7

A:58923

RNA N-glycosidase (EC 3.2.2.22) saporin S9 - common soapwort

C:Species: Saponaria officinalis (common soapwort)

C:Date: 31-Dec-2001 #sequence\_rev:1301 31-Dec-2001 #text\_change:01-Mar-2002

C:Accession: A58923

R:Strattonicola, M.; Di Maro, A.; Ferranti, P.; Bolognesi, A.; Stipe, F.; Parente, submitted to the Protein Sequence Database, December 1998

A:Description: Saporin-S9, the most basic ribosome-inactivating protein from Saponaria

A:Reference number: A58923

A:Accession: A58923

A:Molecule type: protein

A:Residues: 1-253 <MASS>

A:Experimental source: seeds

C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology

C:Keywords: glycosidase; hydrolase; toxin

Query Match 25 38: Score 343.5; DB 2; Length 253;

Best Local Similarity 38.4%; Pred. No. 2,1e-20;

Matches 89; Conservative 42; Mismatches 88; Indels 13; Gaps 7;

OY 2 INTITPDAGNATINKATFMESLRNQAKDPKLCYGIPL-LPDNTSPRYLLVLOGANL 60

Db 1 VTSITLDLVNPTAGQYSSFYDKIRNNWKDPNLKYGCTDIAVIGPSPKDFRLNFQSSR 59

OY 61 KITTLMLRRNNLYVMGYSDPFNGNCKR-YHFNIDITSTERTDVENTLSCSSSRVAMSIN 119

Db 60 GTVSLGLEKRDNLVVAFLAMDNTNVRARAYFRSEITSAEIT---ALFPEATVAANHKALE 115

OY 120 NSLYPMMEKKAEV---NSRNOVOLIQLSDSIGKISGVDSFPKTEAFPLVAIQW 175

Db 116 YTEDYHSIEKNAOITGDKSRKELGLGINILSLSTMTQVANKKRV-VKNDAKRLLIAIQWF 174

OY 176 SEARFKYIENOVKTNFNRAFYPPKVIINLEEKMGKISIAIH-NAKNGALPK 226

Db 175 AEAIVREFYIGNLVTKNPNKFNSENKVIKREVMKKISIAIHGDAANGVFNK 226

RESULT 8

A:505205

RNA N-glycosidase (EC 3.2.2.22) 6 precursor - common soapwort (fragment)

N:Alternate names: ribosome-inactivating protein SO-6, saporin 6

C:Species: Saponaria officinalis (common soapwort)

C:Date: 30-Sep-1991 #sequence\_rev:1301 30-Sep-1991 #text\_change:20-Aug-1999

C:Accession: S05205; A33231; S17689; S16330; A45499

R:Benatti, L.; Saccardo, M.B.; Dani, M.; Nittli, G.; Sassano, M.; Lorenzetti, R.; Latour, J. Biochem. 183, 465-470, 1989

A:Title: Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-inactivating protein from Saponaria

A:Reference number: S05205; M01D:89338421; PMID:2547612

A:Accession: S05205

A:Molecule type: mRNA

A:Residues: 1-283 <BEN>

A:Cross-references: EMBL:X15655

A:Accession: A33231







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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 19,8805 Seconds

(Without alignments)  
730.581 Million cell updates/sec

Title: US-09-978-274a-4\_COPY\_155\_263

Perfect score: 564  
Sequence: 1 GVDSPVKTEAFFLVAIQM.....DEINRDVALLKYNQTCQTT 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	457	81.0	294	AA837345	Pokeweed antiviral
2	454	80.5	224	AAW14255	Mature pokeweed an
3	454	80.5	225	AAW14254	Mature pokeweed an
4	454	80.5	226	AAW14253	Mature pokeweed an
5	454	80.5	227	AAW14252	Mature pokeweed an
6	454	80.5	228	AAW14251	Mature pokeweed an
7	454	80.5	229	AAW14250	Mature pokeweed an
8	454	80.5	230	AAW14249	Mature pokeweed an
9	454	80.5	231	AAW14248	Mature pokeweed an
10	454	80.5	232	AAW14247	Mature pokeweed an

11	454	80.5	233	AAW14246	Mature pokeweed an
12	454	80.5	234	AAW14245	Mature pokeweed an
13	454	80.5	235	AAW14244	Mature pokeweed an
14	454	80.5	236	AAW14243	Mature pokeweed an
15	454	80.5	237	AAW14242	Mature pokeweed an
16	454	80.5	238	AAW14241	Mature pokeweed an
17	454	80.5	239	AAW14240	Mature pokeweed an
18	454	80.5	240	AAW14239	Mature pokeweed an
19	454	80.5	241	AAW14238	Mature pokeweed an
20	454	80.5	242	AAW14237	Mature pokeweed an
21	454	80.5	243	AAW14236	Mature pokeweed an
22	454	80.5	244	AAW14235	Mature pokeweed an
23	454	80.5	245	AAW14234	Mature pokeweed an
24	454	80.5	246	AAW14233	Mature pokeweed an
25	454	80.5	247	AAW14232	Mature pokeweed an
26	454	80.5	248	AAW14231	Mature pokeweed an
27	454	80.5	249	AAW14230	Mature pokeweed an
28	454	80.5	250	AAW14229	Mature pokeweed an
29	454	80.5	251	AAW14228	Mature pokeweed an
30	454	80.5	252	AAW14227	Mature pokeweed an
31	454	80.5	253	AAW14226	Mature pokeweed an
32	454	80.5	254	AAW14225	Mature pokeweed an
33	454	80.5	255	AAW14224	Mature pokeweed an
34	454	80.5	256	AAW14223	Mature pokeweed an
35	454	80.5	257	AAW14222	Mature pokeweed an
36	454	80.5	258	AAW14221	Mature pokeweed an
37	454	80.5	259	AAW14220	Mature pokeweed an
38	454	80.5	260	AAW14219	Mature pokeweed an
39	454	80.5	261	AAW14218	Mature pokeweed an
40	454	80.5	262	AAW14163	Mature pokeweed an
41	454	80.5	262	AAW14164	Mature pokeweed an
42	454	80.5	292	AAW57152	Wild-type Pokeweed
43	454	80.5	292	AAW57153	Pokeweed Antiviral
44	454	80.5	313	AAW8548	Sequence of Phyto
45	454	80.5	313	AAW58025	Wild-type pokeweed

#### ALIGNMENTS

```
RESULT 1
AA837345
ID: AA837345 standard; Protein: 294 AA.
AC: AA837345:
XX
XX 09-NOV-1993 (first entry)
XX
DE Pokeweed antiviral protein.
XX
XX Pokeweed r1c1p; protein synthesis inhibitor; cancer;
XX polymerase chain reaction; PCR.
XX
XX Phytolacca americana.
XX
XX Key
XX Peptide 1..24
XX FT /label= sig-peptide
XX FT 25..294
XX FT /label= mat-protein
XX
XX JF05137580-A.
XX
XX 01-JUN-1993.
XX
XX 20-NOV-1991: 91JP-0329672.
XX
XX 20-NOV-1991: 91JP-0329672.
XX
XX (N1SB ) JAPAN TOBACCO INC.
XX
XX WPI: 1993-211306/26.
XX
XX N-PSDB: AAQ43967.
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XX      New pokeweed antiviral protein (PAP) with similar activity to
PT      ricin - used to treat cancer and as an agricultural chemical
XX
XX      Claim 1: Page 11-13; 14pp; Japanese.
XX
CC      NB: A protein comprising 261 amino acids is claimed.
CC      PAP has a similar activity to ricin, i.e. inhibits protein synthesis.
CC      The protein may be obtained all year round by recombinant DNA
CC      techniques. PAP can be used partic. against cancer and as an
CC      agricultural chemical.
CC      Total mRNA, is extracted from the seeds, leaves and roots of
CC      pokeweed and used to prepare cDNA using PCR. The resultant cDNA is
CC      used to prepare two DNA fractions, which are introduced into a
CC      cloning vector EMBL3 and then into host E.coli PLK-17 (p2) to
CC      produce PAP.
CC
XX      Sequence      294 AA:
SQ
Query Match      81.0%; Score 457; DB 14; Length 294;
Best Local Similarity 82.6%; Pred. No. 7,8e-47;
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0
QY      1 GVDSFVKEAPFLVLAIQMSEARFKYIENQVKTNRNRAFYPPKYNILEEKWKISE 60
Db      177 GVDSFTEKTEAEFLVAIQMSEARFKYIENQVKTNRNRAFYPPAKYLNLEESWGKIST 236
QY      61 AIHNANNGALPKPELVDAKGTKMIVLRVDEINRDVALTKVNGTCOTT 109
Db      237 AIHNANNGALTSPELEKNNAGSKWIVLRVDIPEVGLTKVNGTCOAT 285

RESULT 2
AAAI4255
ID      AAMI4255 standard; protein; 224 AA.
XX
AC      AAMI4255:
XX
DT      25-JUN-1997 (first entry)
XX
DE      Mature pokeweed antiviral protein deletion variant (39-262).
XX
KW      Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KW      anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW      stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KW      translation; broad spectrum; resistance; cell death; sterility; nematode;
KW      bacterium.
XX
KM      Phytolacca americana.
XX
OS      Phytolacca americana.
XX
PN      MO9703183-A1.
XX
PD      30-JAN-1997.
XX
PE      11-JUL-1996; 96MO-US11546.
XX
PF      11-JUL-1995; 95US-0500694.
XX
PR      11-JUL-1995; 95US-0500611.
XX
PA      (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI      Turner NE;
XX
WPt: 1997-119040/11.
XX
PT      New pokeweed antiviral protein mutants - which exhibit anti-viral
PT      and anti-fungal activity in plants and have reduced phytotoxicity
XX
XX      Claim 14: -: 64pp; English.
XX
CC      Proteins AAMI4163-414256 represent new pokeweed antiviral protein (PAP)
CC      mutants having reduced phytotoxicity but retaining anti-viral or
CC      anti-fungal activity in plants. The sequences' numbering corresponds to

```

CC	the 262 amino acid mature protein. The proteins AAM14165-W14217
CC	represent serial deletions from the C-terminus whereas sequences
CC	AAM14218-55 are serial deletions from the N-terminus. Prior to
CC	processing, the protein contains a 22 amino acid N-terminal signal
CC	sequence and a 29 amino acid C-terminal extension. PAP is a Type I
CC	ribosomal inhibitor protein (RIP) that catalyses the removal of a
CC	specific adenine residue from a highly conserved stem-loop structure in
CC	the 26S rRNA of eukaryotic ribosomes and also interferes with elongation
CC	factor-2 binding thus blocking protein translation. The PAP mutants can
CC	confer broad spectrum virus and fungus resistance to plants without
CC	causing plant cell death or sterility. They can also confer increased
CC	resistance to insects, bacteria and nematodes in plants.
CC	N.B. This sequence is not given in the specification but is generated
CC	from the wild type sequence reproduced in the specification.
XX	
SO	Sequence 224 AA:
QY	Query Match 80.5%, Score 454, DB 18, Length 224;
Db	Best Local Similarity 82.6%, Pred. No.1.2e-46;
	Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY	1 GVDSFPVTEAFPLFLVAIQMYSSEARFYIENQVTFNRFAPDPKVIINLEEKWKISE 60
Db	116 GVMSFTEKTEAEFLFLVAIQMYSSEARFYIENQVTKTNRRAFNPPKVLNLQETWGIKIST 175
QY	61 AIHNKAGCALPKPLELYDAKGTKWLIVLRVDEINRDVALLLKYNGTCQPT 109
Db	176 AIHDAKNQVLPRPLELYDASGAKWILRVDEIKRPDVALLVYGGSCQPT 224
RESULT 3	
AAM14254	
ID	AAM14254 standard; protein: 225 AA.
XX	
AC	AAM14254;
XX	
DT	25-JUN-1997 (first entry)
XX	
DE	Mature pokeweed antiviral protein deletion variant (38-262).
XX	
KW	Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KW	anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW	stem-loop; 26S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KW	translation; broad spectrum; resistance; cell death; sterility; nematode;
KW	bacterium.
XX	
OS	Phytolacca americana.
XX	
PN	WO9703183-A1.
XX	
PD	30-JAN-1997.
XX	
PE	11-JUL-1996; 96WO-US11546.
XX	
PR	11-JUL-1995; 95US-0500694.
XX	
PR	11-JUL-1995; 95US-0500611.
XX	
PA	(RUTP ) UNIV RUTGERS STATE NEW JERSEY.
XX	
PL	Turner NE;
XX	
DR	WPI: 1997-119040/11.
XX	
PT	New pokeweed antiviral protein mutants - which exhibit anti-viral
XX	and anti-fungal activity in plants and have reduced phytotoxicity
XX	
PS	Claim 14: -; 64pp: English.
XX	
CC	Proteins AAM14165-W14256 represent new pokeweed antiviral protein (PAP)
CC	mutants having reduced phytotoxicity but retaining anti-viral or
CC	anti-fungal activity in plants. The sequences' numbering corresponds to
CC	the 262 amino acid mature protein. The proteins AAM14165-W14217
CC	represent serial deletions from the C-terminus whereas sequences



CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX Sequence 225 AA:

Query Match 80.5%; Score 454; DB 18; Length 225;  
 Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSPVKTAEFFLLVAIQMSEARFKYIENOVKTNFRAPYPPKVINLEKKKISF 60  
 DB 117 GVMSTFKTEAEFFLLVAIQMSEARFKYIENOVKTNFRAPYPPKVINLEKKKIST 176  
 OY 61 AIHNAKNGALPKPDELVDKAKTKWIVLRVDEINRVALLKYNGTCQTT 109  
 DB 177 AIHDAKNGVLPKPLELDVDSGAKWIVLRVDEIKPVDALLNYGSCQTT 225

#### RESULT 4

AAM14253  
 ID AAM14253 standard; protein: 226 AA.

XX AAM14253:

DT 25-JUN-1997 (first entry)

XX Mature pokeweed antiviral protein deletion variant (37-262).

XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 XX anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 XX stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 XX translation; broad spectrum; resistance; cell death; sterility; nematode;  
 XX bacterium.

OS Phytolacca americana.

PN WO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Tumor NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 and anti-fungal activity in plants and have reduced phytoxicity

XX Claim 14: -: 64pp; English.

XX Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal

CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX Sequence 226 AA:

Query Match 80.5%; Score 454; DB 18; Length 226;  
 Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSPVKTAEFFLLVAIQMSEARFKYIENOVKTNFRAPYPPKVINLEKKKISF 60  
 DB 118 GVMSTFKTEAEFFLLVAIQMSEARFKYIENOVKTNFRAPYPPKVINLEKKKIST 177  
 OY 61 AIHNAKNGALPKPDELVDKAKTKWIVLRVDEINRVALLKYNGTCQTT 109  
 DB 178 AIHDAKNGVLPKPLELDVDSGAKWIVLRVDEIKPVDALLNYGSCQTT 226

#### RESULT 5

AAM14252  
 ID AAM14252 standard; protein: 227 AA.

XX AAM14252:

DT 25-JUN-1997 (first entry)

XX Mature pokeweed antiviral protein deletion variant (36-262).

XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 XX anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 XX stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 XX translation; broad spectrum; resistance; cell death; sterility; nematode;  
 XX bacterium.

OS Phytolacca americana.

PN WO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX Tumor NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 and anti-fungal activity in plants and have reduced phytoxicity

XX Claim 14: -: 64pp; English.

XX Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
 CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a

CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX Sequence 227 AA.

Query Match 80.5%; Score 454; DB 18; Length 227;  
 Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSEPVKTEAFLLVAIQMVSSEARFYIENQVKTNNRAFYPPDKYINLEEKKGISE 60  
 DB 119 GVMSTFEKTEAEFLVAIQMVSSEARFYIENQVKTNNRAFPKPLNLEETWKGIST 178  
 OY 61 AIHNKNGALPKPLVDKGTWVLRVDEINRVALLLKYNGTCQTT 109  
 DB 179 AIHDAKNGVLPKPLVDASGAKWIVLRVDEIKPVALNLYVGGSCQTT 227

RESULT 6

AAM14251

ID AAM14251 standard; protein: 228 AA.

XX AAM14251;

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (35-262).

XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KW bacterium.

XX PhytoIacca americana.

XX MO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTE ) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI; 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 PT and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14; -: 64pp; English.

XX Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation

CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX Sequence 228 AA.

Query Match 80.5%; Score 454; DB 18; Length 228;  
 Best Local Similarity 82.6%; Pred. No. 1.3e-46;  
 Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 1 GVDSEPVKTEAFLLVAIQMVSSEARFYIENQVKTNNRAFYPPDKYINLEEKKGISE 60  
 DB 120 GVMSTFEKTEAEFLVAIQMVSSEARFYIENQVKTNNRAFPKPLNLEETWKGIST 179  
 OY 61 AIHNKNGALPKPLVDKGTWVLRVDEINRVALLLKYNGTCQTT 109  
 DB 180 AIHDAKNGVLPKPLVDASGAKWIVLRVDEIKPVALNLYVGGSCQTT 228

RESULT 7

AAM14250

ID AAM14250 standard; protein: 229 AA.

XX AAM14250;

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (34-262).

XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
 KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
 KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 KW bacterium.

XX PhytoIacca americana.

XX MO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTE ) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI; 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 PT and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14; -: 64pp; English.

XX Proteins AAM14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAM14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAM14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without







Db 127 GWSFTEKTEAEFLVAIOMVSEARFKYIENOVKTNFRARNPNKRVNLDETCKIST 186  
QY 61 AIHNKNGALPKPLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 109  
Db 187 AIHDAKNVLPKPLELDVDAKGTWIVLRVDEIKPVDALLNTVGGSCQTT 235

## RESULT 14

AAW14243  
ID AAW14243 standard; protein; 236 AA.

AC AAW14243;

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (27-262).

KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.

OS Phytolacca americana.

PN MO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96MO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
PR and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14: -; 64bp; English.

CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

SQ Sequence 236 AA;

Query Match 80.5%; Score 454; DB 18; Length 236;

Best Local Similarity 82.6%; Pred. No. 1.3e-46; Mismatches 14; Indels 0; Gaps 0;

QY 1 GVDSPVKTAEAFLLVAIOMVSEARFKYIENOVKTNFRARYPDPKVINLEKWKIS 60  
Db 128 GWSFTEKTEAEFLVAIOMVSEARFKYIENOVKTNFRARNPNKRVNLDETCKIST 187

QY 61 AIHNKNGALPKPLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 109  
Db 188 AIHDAKNVLPKPLELDVDAKGTWIVLRVDEIKPVDALLNTVGGSCQTT 236

## RESULT 15

AAW14242  
ID AAW14242 standard; protein; 237 AA.

AC AAW14242;

DT 25-JUN-1997 (first entry)

DE Mature pokeweed antiviral protein deletion variant (26-262).

KW Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.

OS Phytolacca americana.

PN MO9703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96MO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
PR and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14: -; 64bp; English.

CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

SQ Sequence 237 AA;

Query Match 80.5%; Score 454; DB 18; Length 237;

Best Local Similarity 82.6%; Pred. No. 1.3e-46; Mismatches 14; Indels 0; Gaps 0;

QY 1 GVDSPVKTAEAFLLVAIOMVSEARFKYIENOVKTNFRARYPDPKVINLEKWKIS 60  
Db 129 GWSFTEKTEAEFLVAIOMVSEARFKYIENOVKTNFRARNPNKRVNLDETCKIST 188  
QY 61 AIHNKNGALPKPLELDVDAKGTWIVLRVDEINRDVALLKYVNGTCQTT 109

Db 189 A1HDAKNGVLPKPLEVDASGAKWILRVDEIKPPDVALLNYYGSGCOTT 237

Search completed: July 2, 2003, 11:39:41  
Job time : 20.8805 secs





PT and for targeted cell destruction  
 XX Claim 10, Fig 1, 25pp: French.  
 PS  
 CC Mutants of type I Ribosome Inactivating Proteins which are toxic to  
 CC eukaryotic, but not prokaryotic, cells.  
 CC the wild-type Pokeweed Antiviral Protein (PAP) is preferably derived from  
 CC Arg at position 68) and PAP9 (with Gly replacing wild-type Phe and  
 CC Arg replacing wild-type Lys at positions 196 and 211, respectively).  
 XX Sequence 292 AA;  
 SO  
 Query Match  
 Best Local Similarity 75.8%; Score 601; DB 15; Length 292;  
 Matches 111; Conservative 23; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MINTTFDAGNATINKYATFMSLRNOADPKLCYGPMLPDTNSTPKYLLVLOCANL 60  
 DB 1 VNTIIIVGSTTISKYATFPLNDLRNEADPKSLKCYGIPMLPNTNTPKYLVLVELOGSNK 60  
 QY 61 KTTTLMRRNNLYVMGYSDPFNGNCRHYIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 DB 61 KTTTLMRRNNLYVMGYSDPFNGNCRHYIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 QY 121 NSLYPTMEKKAENVSRNOVOLGQIILSDIGKIS 154  
 DB 121 DSRVPTLESKAGVKSRSQVQIGIQLDSDIGKIS 154  
 RESULT 10  
 AAW14217 standard; protein: 184 AA.  
 ID AAW14217  
 AC AAW14217  
 XX 25-JUN-1997 (first entry)  
 DT XX  
 DE Mature pokeweed antiviral protein deletion variant (1-184).  
 XX Pokeweed antiviral protein deletion variant (1-184).  
 KW anti-fungal; fungus; mutant: phytoxicity; anti-viral; virus;  
 KW stem-loop; 28S rRNA; plant; ribosomal inhibitor protein; adenine; insect;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 XX bacterium.  
 OS Phytotheca americana.  
 PN M09703183-A1.  
 PD 30-JAN-1997.  
 XX 11-JUL-1996; 96MO-US11546.  
 PR 11-JUL-1995; 95US-0500694.  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 PI Turner NE;  
 DR WPI: 1997-119040/11.  
 PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 XX and anti-fungal activity in plants and have reduced phytotoxicity  
 PS Claim 8; -; 64pp: English.  
 CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC anti-fungal activity reduced phytotoxicity but retaining anti-viral  
 CC the 262 amino acid mature protein. The sequences, numbering corresponds to  
 CC represent serial deletions from the C-terminus whereas sequences

us-09-978-274a-6.rag  
 CC AAW14218-55 are serial deletions from the N-terminus.  
 CC processing, the protein contains a 22 amino acid N-term.  
 CC sequence and a 29 amino acid C-terminal extension.  
 CC ribosomal inhibitor protein (RIP) that catalyzes the  
 CC the 28S rRNA of eukaryotic from a highly conserved stem-  
 CC factor-2 binding thus blocking ribosomes and also interfere  
 CC causing broad spectrum virus and fungus resistance. The  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC from the wild type sequence reproduced in the specification.  
 XX Sequence 184 AA;  
 SO  
 Query Match  
 Best Local Similarity 71.9%; Score 596; DB 18; Length 184;  
 Matches 110; Conservative 23; Mismatches 20; Indels 0;  
 QY 2 INTTFDAGNATINKYATFMSLRNOADPKLCYGPMLPDTNSTPKYLLVLOCANL 60  
 DB 1 VNTIIIVGSTTISKYATFPLNDLRNEADPKSLKCYGIPMLPNTNTPKYLVLVELOGSNK 60  
 QY 62 TTTTLMRRNNLYVMGYSDPFNGNCRHYIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 DB 62 TTTTLMRRNNLYVMGYSDPFNGNCRHYIFNDISTERTDVENTLSSSSSRVAMSTNY 120  
 QY 121 NSLYPTMEKKAENVSRNOVOLGQIILSDIGKIS 154  
 DB 121 DSRVPTLESKAGVKSRSQVQIGIQLDSDIGKIS 154  
 RESULT 11  
 AAW14216 standard; protein: 185 AA.  
 ID AAW14216  
 AC AAW14216  
 XX 25-JUN-1997 (first entry)  
 DT XX  
 DE Mature pokeweed antiviral protein deletion variant (1-185).  
 XX Pokeweed antiviral protein deletion variant (1-185).  
 KW anti-fungal; fungus; mutant: phytoxicity; anti-viral; virus;  
 KW stem-loop; 28S rRNA; plant; ribosomal inhibitor protein; adenine; insect;  
 KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
 XX bacterium.  
 OS Phytotheca americana.  
 PN M09703183-A1.  
 PD 30-JAN-1997.  
 XX 11-JUL-1996; 96MO-US11546.  
 PR 11-JUL-1995; 95US-0500694.  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 PI Turner NE;  
 DR WPI: 1997-119040/11.  
 PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 XX and anti-fungal activity in plants and have reduced phytotoxicity  
 PS Claim 8; -; 64pp: English.  
 CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC anti-fungal activity reduced phytotoxicity but retaining anti-viral  
 CC the 262 amino acid mature protein. The sequences, numbering corresponds to  
 CC represent serial deletions from the C-terminus whereas sequences



	Query Match	36.8%	Score 207.5;	DB 10;	Length 279;	
	Best Local Similarity	47.4%;	Pred No. 3;9e-14;			
	Matches 46;	Conservative 15;	Mismatches 29;	Indels 7;	Gaps 2	
Oy	8 KTEAFFLLVAALQWSEARFRFYIENQ--VKTNFNRAFPDPKVINLEEKWKGISIAIHNA 65                                 :       :       187 KTEARFLLIALQWAEARFRFYIGRAIVTTAPN-----DKHILSLENNMGALSIGIRNA 241					
Db	66 KNGALPKPLELVDAKGTKWIVLRVDINRDVALLKYV 102 :       :       :       :       :       :       242 VKKVINPEITLQYPDGKWIVTQVSDVKNMGDLKKYV 278					
RESULT 12						
ID	PRELIMINARY:	PRT:	279 AA.			
09AUE3						
AC	09AUE3:					
DT	01-JUN-2001 (TREMBLrel. 17, Created)					
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)					
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)					
DE	rRNA_glycosidase (EC 3.2.2.22).					
CAP30B.						
OS	Chenopodium album (lamb's-quarters).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium. NCBI_TaxID=33559;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RK	Park J.S., Lee S.M., Kim Y.T., Cho K.J.;					
RT	"Molecular characterization of a new cDNA clone encoding a ribosome-					
RL	inactivating protein (CAP30B) from Chenopodium album ";					
RT	Submitted (Feb-2000) to the EMBL/Genbank/DDJ databases.					
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE					
CC	SPECIFIC ADENOSINE ON THE 28S RNA.					
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.					
DR	EMBL: AF230812; AAK28323.1; -					
DR	HSSP: Q03464; IAPA.					
DR	InterPro: IPR001574; RIP.					
DR	Pfam: PF00161; RIP.1.					
DR	PRINTS: PRO0396; SHIGARICIN.					
KW	Hydrolase; Toxin..					
SO	SEQUENCE 279 AA; 31419 MW; 97E934F22C8033AF CRC64;					
Query Match	35.0%;	Score 197.5;	DB 10;	Length 279;		
Best Local Similarity	45.4%;	Pred No. 4;6e-13;				
Matches 44;	Conservative 17;	Mismatches 29;	Indels 7;	Gaps 2		
Oy	8 KTEAFFLLVAALQWSEARFRFYIENQ--VKTNFNRAFPDPKVINLEEKWKGISIAIHNA 65                                 :       :       187 KTEARFLLIALQWAEARFRFYIGRAIVTTAPN-----NKIYSLLENMGALSIGIRNA 241					
Db	66 KNGALPKPLELVDAKGTKWIVLRVDINRDVALLKYV 102 :       :       :       :       :       :       242 VKKVINPEITLQYPDGKWIVTQVSDVKNMGDLKKYV 278					
RESULT 13						
ID	PRELIMINARY:	PRT:	541 AA.			
041174						
AC	041174:					
DT	01-NOV-1996 (TREMBLrel. 01, Created)					
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	rRNA_glycosidase (EC 3.2.2.22) (Fragment).					
OS	Rhizinus communis (Castor bean).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Eurosids I; Malpighiales; Euphorbiales; Euphorbiaceae; Rhizinus. NCBI_TaxID=3988;					
RN	[1]					
RP	SEQUENCE FROM N.A.					

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RA MEDLINE=92338377; PubMed=1633311.
RX Roberts L.W., Tregear J.W., Lord J.M.;
RT "Molecular cloning of ricin".
RL Targeted Diagn. Ther. 7:81-97(1992).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: S40366; AAB22582.1; -.
DR HSSP: P02879; 1BR6.
DR InterPro: IPR000772; Ricin_B_lectin.
DR InterPro: IPR001574; RIP.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00652; Ricin_B_lectin; 6.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR SMART: SMO0458; RICIN; 2.
DR PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
DR PROSITE: PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KM Hydrolase; Toxin.
FT NON_TER
SO SEQUENCE 541 AA; 60281 MW; 287B2CDEF1F2E9D9 CRC64;

Query Match 34.0%; Score 192; DB 10; Length 541;
Best Local Similarity 39.8%; Pred. No. 4.1e-12;
Matches 41; Conservative 19; Mismatches 39; Indels 4; Gaps 2;

QY 1 GVDSFPVTEAFFLVLAQVNSAARFYENQVKT--NFNRAFPDPKVINLEEKWKI 58
DB 157 GGTOPLTARSF--IICQIMSEARFPYIGENKTRIRYRRASPDPSVITLSEMSORL 214
QY 59 SEAIHNAKNGALPKPLELVDAKGTKWIVLRVDEINRDVALKY 101
DB 215 STAIQESNOGAFASPIQLORRNGSKFYSVDYSILPIALAMY 257

RESULT 14
QBW4U4 PRELIMINARY: PRT: 305 AA.
ID QBW4U4 AC
AC QBW4U4:
DT 01-MAR-2002 (TREMBLrel. 20, created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Bouganin.
OS BouganinVlaa spectabilis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Nyctaginaceae; BouganinVlaa.
OX NCBI_TaxID=146096;
RX (1)
RN SEQUENCE FROM N.A.
RP de Haerig M.T., Lubelli C., Boon L., Heerkens S., Oltiz Buijsse A.P.,
RA den Boer M., Stijpe F.
RT "Cloning and expression of cDNA coding for bouganin: A type I
RT ribosome-inactivating protein from BouganinVlaa spectabilis Willd.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF445416; AAL3962.1; -.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
SO SEQUENCE 305 AA; 34067 MW; 31505CE91962DCDB CRC64;

Query Match 33.4%; Score 188.5; DB 10; Length 305;
Best Local Similarity 43.6%; Pred. No. 4.8e-12;
Matches 41; Conservative 18; Mismatches 32; Indels 3; Gaps 2;

QY 11 AFFLVLAQVNSAARFYENQ--VKTNFNRAFPDPKVINLEEKWKISEAHINA--KN 67
DB 179 AKFLVIAQVNSAARFYETEVVDRLGVSFKPNFVLNLNNMGQISDAIHKSSPQC 238
QY 68 GALKPLELVDAKGTKWIVLRVDEINRDVALKY 101

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09S9E4
ID 09S9E4 PRELIMINARY: PRT: 258 AA.
AC 09S9E4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE rRNA - glycosylase (EC 3.2.2.22).
OS Geonium multiflorum (Euphorbiaceae himalayae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Malpighiales; Euphorbiaceae; Geonium.
OX NCBI_TaxID=3979;
RN (1)
RP SEQUENCE.
RX MEDLINE=96006751; PubMed=7553224;
RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
RA Toman P.D., Cheung L.;
RT "Amino acid sequence analysis, gene construction, cloning, and
RT expression of geonium, a toxin derived from Geonium multiflorum.";
RL J Interferon Cytokine Res. 15:547-555(1995).
-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
CC HSSP: P09989; IMRJ.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolyase; Toxin.
SO SEQUENCE 258 AA; 28826 MW; 13068E673F4D6B06 CRC64;

Query Match 37.7%; Score 212.5; DB 10; Length 258;
Best Local Similarity 44.7%; Pred. No. 1e-14; Mismatches 36; Indels 1; Gaps 1
Matches 46; Conservative 18;

QY 2 VDSEPVKTEAEFFLLVAIQMVSEARFKYKTIENQVKTNFRAFPDPKVINLEKWKGISIA 61
DB 152 IDNKKPTEIASLLVVIQMVSEARFTIENGRNNFOGRIPANNNTISLEKWKGLSPQ 211
QY 62 IH-NKNGALPKPLELVDAKGTKIVLVKDELINRDAVALLKYN 103
DB 212 IRTSGANGMFESEVLELERRANGKRYVTVADQVKPKIALLKFDV 254

RESULT 11
ID 09M5K6 PRELIMINARY: PRT: 279 AA.
AC 09M5K6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE rRNA - glycosylase (EC 3.2.2.22).
OS Geonium multiflorum (Euphorbiaceae himalayae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
OX NCBI_TaxID=3559;
RN (1)
RP SEQUENCE FROM N.A.
RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;
RT "A cDNA clone encoding a novel ribosome inactivating protein from
RT Chenopodium album L.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
CC EMBL: AF228508; AAF66234.1; -.
DR HSSP: C03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PRINTS: PR00396; SHIGARICIN.
KW Hydrolyase; Toxin.
SO SEQUENCE 279 AA; 31377 MW; 2A53300EA45DC952 CRC64;

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RL Plant Mol. Biol. 43:439-450(2000).  
 CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC EMBL: AF141331; AAD32679.1; -.  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PRO0396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; UNKNOWN\_1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 315 AA; 35728 MW; F85DE2115A85FA15 CRC64;

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Query Match      77.5%: Score 437: DB 10: Length 315;
Best Local Similarity 78.9%: Pred. No. 1.le-38;
Matches 86: Conservative 7: Mismatches 16: Indels 0: Gaps 0

QY 1 GVDSEPVKTEAFLLVIAIQWYSEARAFYIENQVKTNFNRAFYPPDKVINLEEKMKISE 60
   |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 GVDVPEKTEAFLLVIAIQWYSEARAFYIENQVKTNFNRAFYPPDKVINLEETWKIST 238
   |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 AIHNAKNGALPKPLELVDAKSTKIVLRVDEINRDVALLKLYNGTCQQT 109
   |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 AIHNAKNGALTKPLELINEDGSKIVLRVDEIKPDVGLLVNYDGCQQT 287
   |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT	6
Q8S947	
ID	Q8S947
AC	Q8S947;
DT	01-JUN-2002 (TReMBLrel. 21, Created)
DT	01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE	PAP-S1 (Fragment).
GN	PAP.S1.
OS	Phytolacca americana (Common pokeweed).
OC	Eudaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;
OC	Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OX	NCBI_TaxID=35227;
ON	111

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RP  SEQUENCE FROM N.A.
RA  Honjo E., Watanabe K.;
RT  "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT  protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT  their recombinant proteins with other PAP isoforms. ";
RL  Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB071854; BAB86349.1; -.
DT  NON_TER      1
FT  NON_TER      261
SQ  SEQUENCE      261 AA;  29199 MW;  D8B9B98BFE1F989 CXC64;

Query Match      76.1%;  Score 429;  DB 10;  Length 261;
Best Local Similarity 78.9%;  Pred. No. 6,4e+38;
Matches 86;  Conservative 5;  Mismatches 18;  Indels 0;  Gaps 0

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DE	Q9ATB3	PRELIMINARY;	PRT;	237 AA.
QY	1	GVGSFPAKTAFFFLVAIQWVSEARRRKIYENQKTNENRFAFYDPDKVILNEEKWKIS	60	
Db	153	GGCSFTEKIEAKFLVAIQWVSEARRRKIYENQKTNENRDFSPNDKVLDEENMGKIST	212	
QY	61	AIHNAKNGALPKPELVDAKGTKIVLRVDEINRDVALIKYVNGTCQTT	109	
Db	213	AIHNSKNGALPKPELKNADGKTIYLRVDEIKPDDVGLINYNCTQAT	261	
RESULT 7				
ID	Q9ATB3	PRELIMINARY;	PRT;	237 AA.
AC	Q9ATB3;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	TRNA-glycosidase (EC 3.2.2.22) (Fragment).			

GN	M.P.A.
OS	Phytolacca americana (Common pokeweed) .
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Caryophyllales; Caryophyllaceae; Phytolacca.
OX	NCBI_TaxID=35327;
RN	(1)
RP	SEQUENCE FROM N.A.
RA	Chen D., Wang X., Zhou G.;
RT	"Pokeweed antiviral protein gene, partial cds.";
RL	Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
CC	-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.
CC	-I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR	EMBL: AF338910; AAK21951.1; -
DR	HSSP; P10297; 10CG.
DR	InterPro; IPR001574; RIP.
DR	Pfam; PF00161; RIP; 1.
DR	PRINTS; PRO0396; SHIGARICIN.
DR	PROSITE; PS00275; SHIGA_RICIN; 1.
KW	Hydrolase; Toxin.
FT	NON_TER 1
FT	NON_TER 237
SQ	SEQUENCE 237 AA: 26534 MW: FEADACEE03464783 CRC64:

[illegible]

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RESULT 8
ID P93077 PRELIMINARY; PRT; 302 AA.
AC P93077;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE rRNA_glycosidase (EC 3.2.2.22).
GN RIP.
OS Clerodendrum aculeatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiales; Clarendendrium.
OX NCBI_TaxID=54206;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=LEAF;
RX MEDLINE=97238481; Pubmed=9132066;
RA Kumar D., Verma H.N., Tuteja N., Tewari K.K.;
RT Cloning and characterisation of a gene encoding an antiviral protein
RT from Clerodendrum aculeatum L.";
RL Plant Mol. Biol. 33:745-751(1997).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 26S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
EMBL X96447; CAA65328.1; -;
DR EMBL; X96583; CAA65402.1; -;
DR HSSP; P10297; IQCG.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP. 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Glycosidase; Hydrolase; Toxin.
SQ SEQUENCE 302 AA; 33955 MW; B0561C3918C2E6A2 CRC64;

```

QY 1 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 60  
DB 178 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 237  
QY 61 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 109  
DB 238 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 286

RESULT 2  
08S946 PRELIMINARY: PRT: 262 AA.  
ID 08S946  
AC 08S946  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE PAP-S2 (Fragment).  
GN PAP-S2.  
OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Honjo E., Matanabe K.:  
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral  
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of  
RT their recombinant proteins with other PAP isoforms."  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB071855; BAB86350.1; -  
FT NON\_TER 1 262  
FT SEQUENCE 262 AA; 29486 MW; AF2D010A73C9D1B8 CRC64;  
SQ

Query Match 99.1%; Score 559; DB 10: Length 262;  
Best Local Similarity 99.1%; Pred. No. 7.4e-52;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 60  
DB 154 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 213

QY 61 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 109  
DB 214 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 262

RESULT 3  
0941G8 PRELIMINARY: PRT: 313 AA.  
ID 0941G8  
AC 0941G8  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE rRNA - glycosidase (EC 3.2.2.22).  
GN PAP.  
OS Phytolacca acinosa.  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
OX NCBI\_TaxID=107615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Peng X., Yuan J., Qiang B.:  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC -1- SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -1- STIMULATORY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
DR EMBL: AY049785; AAL15442.1; -  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP; 1.

KM Hydrolase: Toxin.  
SQ SEQUENCE 313 AA; 35059 MW; E478ECD571C17885 CRC64;  
QY 1 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 60  
DB 176 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 235

QY 61 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 109  
DB 236 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 284

RESULT 4  
08RYA4 PRELIMINARY: PRT: 339 AA.  
ID 08RYA4  
AC 08RYA4  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Ribosome inactivating protein type 1 precursor.  
OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.:  
RT "Characterization of a novel ethylene-inducible ribosome-inactivating  
RT protein exuded from root cultures of Phytolacca americana."  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY071928; AAL61546.1; -  
FT SIGNAL 1 47  
FT SIGNAL. POTENTIAL.  
FT SEQUENCE 339 AA; 37978 MW; 7D47BDCDEDD965F CRC64;  
SQ

Query Match 77.7%; Score 438; DB 10: Length 339;  
Best Local Similarity 80.4%; Pred. No. 9.6e-39;  
Matches 86; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 60  
DB 203 GVDSFPVKTEAFLLVAIQVSEARPKYIENOVKTENFRAFPDPKVINLEEKWKISF 262

QY 61 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 107  
DB 263 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKYVNGTCTT 309

RESULT 5  
09XF8 PRELIMINARY: PRT: 315 AA.  
ID 09XF8  
AC 09XF8  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE rRNA - glycosidase (EC 3.2.2.22).  
GN PIP2.  
OS Phytolacca insularis.  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
OX NCBI\_TaxID=63744;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=20505377; PubMed=11052196;  
RA Song S.K., Choi Y., Moon Y.H., Kim S.G., Choi Y.D., Lee J.S.:  
RT "Systemic induction of a Phytolacca insularis antiviral protein gene  
RT by mechanical wounding, jasmonic acid, and abscisic acid".

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 15.7673 Seconds

(without alignments)  
1424.413 Million cell updates/sec

Title: us-09-978-274a-4\_COPY\_155\_263

Sequence: 564  
1 GVDSFPYKTEAFFLVAIQM.....DEINRDVALLKYNCTCQT 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_rvivirus:\*  
17: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564	100.0	314	10	P93444
2	559	99.1	262	10	O85946
3	449	79.6	313	10	O941G8
4	438	77.7	339	10	O8RYA4
5	437	77.5	315	10	O9XFF8
6	429	76.1	261	10	O8S947
7	355	62.9	237	10	O9ATB3
8	302	53.5	302	10	P93077
9	215	38.1	272	10	O93418
10	212.5	37.7	258	10	O9S9E4
11	207.5	36.8	279	10	O9S9E4
12	197.5	35.0	279	10	O9AUE3
13	192	34.0	541	10	O41174
14	188.5	33.4	305	10	O8W4U4
15	170.5	30.2	294	10	O93Y65
16	170.5	30.2	294	10	O93Y64

17	154.5	27.4	294	10	O93Y66	O93Y66 dianthus ch
18	149	26.4	289	10	P93261	P93261 mesembryant
19	147.5	26.2	549	10	O9EV22	O9EV22 cinanomom
20	147.5	26.2	580	10	O94BW3	O94BW3 cinanomom
21	147.5	26.2	581	10	O94BW5	O94BW5 cinanomom
22	146.5	26.0	270	10	O9SA05	O9SA05 amarantus
23	146.5	26.0	319	10	O8VWY2	O8VWY2 spinacia ol
24	146	25.9	289	10	O94KE4	O94KE4 trichosan
25	145	25.7	247	10	O9LRE3	O9LRE3 trichosan
26	145	25.7	289	10	O41216	O41216 trichosan
27	145	25.7	382	10	O8SA43	O8SA43 abrus preca
28	144	25.5	270	10	O41611	O41611 trichosan
29	143.5	25.4	279	10	O9ZRT5	O9ZRT5 amarantus
30	143.5	25.4	284	10	O96322	O96322 amarantus
31	143.5	25.4	580	10	O94BW4	O94BW4 cinanomom
32	138	24.5	293	10	O8VYU0	O8VYU0 jatropa cu
33	137.5	24.4	251	10	O48859	O48859 amarantus
34	137.5	24.4	278	10	O00980	O00980 luffa cylin
35	137	24.3	286	10	O9FUV7	O9FUV7 momordica c
36	135	23.9	252	10	O38761	O38761 abrus preca
37	134	23.8	565	10	O04071	O04071 sambucus n
38	134	23.8	566	10	O04072	O04072 sambucus n
39	133.5	23.7	604	10	O9M654	O9M654 jatropa cu
40	133	23.6	293	10	O9M652	O9M652 jatropa cu
41	133	23.6	547	10	O9M6E9	O9M6E9 abrus preca
42	132.5	23.5	570	10	O22415	O22415 sambucus n
43	132.5	23.5	603	10	O9M653	O9M653 polygonatum
44	132	23.4	264	10	O9F5H2	O9F5H2 momordica c
45	132	23.4	286	10	O41257	O41257 momordica c

## ALIGNMENTS

RESULT 1  
P93444 PRELIMINARY; PRT; 314 AA.  
ID P93444  
AC P93444  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE rRNA - glycosidase precursor (EC 3.2.2.22).  
GN PAP-S.  
OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED;  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J.L., Hoeveler A.;  
RT "cDNA cloning of the gene encoding the Antiviral protein from the  
RT seeds of Phytolacca americana and its expression in E.coli.";  
RL FEBS Lett. 406:97-100(1997).  
CC -|- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC -|- SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -|- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
CC EMBL: X98079; CA66702.1;  
DR HSSP: O03464; IAPA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.1.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
FT HYDROLASE; Signal; Toxic.  
FT SIGNAL 1 24  
FT CHAIN 25 314 POTENTIAL.  
SQ SEQUENCE 314 AA; 35323 MW; A89E3CE57789F9E CRC64;  
Query Match 100.0%; Score 564; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 2.7e-52;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 VNTIIYVNGSTTISKYATFLNDRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKK 82  
QY 62 TITLMLRRNNLYVWGSDPENGKCRHYIENDISTERTDYENTLSSSSSRVAMSTINY 121  
Db 83 TITLMLRRNNLYVWGSDPENGKCRHYIENDISTERTDYENTLSSSSSRVAMSTINY 142  
QY 122 SLVPTMEKKAEVNSRNOVOLGIIQLSSDICKISGVDSFPVYTEAFLLVAIQWSEARF 181  
Db 143 SRYPTELESKAGVKSRSOVOLGIIQLSSDICKISGVDSFPVYTEAFLLVAIQWSEARF 202  
QY 182 KYIENOVKTNNRAFNPPKVINLEEKWKISEAIHNAKNGALPKPLELVDAGKTKWIVL 241  
Db 203 KYIENOVKTNNRAFNPPKVINLEETWGIKISTAIHDAKNGVLPKPLELVDAGAKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 263 RVDEIKPDVALLNIVGGSCOTT 284

## RESULT 15

US-08-500-694-2

Sequence 2, Application US/08500694

Patent No. 5880329

GENERAL INFORMATION:

APPLICANT: Tumer, Nilgun E.

TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein

TITLE OF INVENTION: Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lerner, David, Littenberg, Krumholz &amp; Menclik

STREET: 600 South Avenue West

CITY: Westfield

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/500,694

FILING DATE: 11-JUL-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REFERENCE/DOCKET NUMBER: OCIRS 3.0-039

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000

TELEFAX: 908-654-7866

TELEX: 139-125

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-500-694-2

Query Match 77.4%; Score 1050; DB 2; Length 313;

Best Local Similarity 76.3%; Pred. No. 5,4e-100;

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 2 INTITFDAGNATINKYATFMESLRNOAKDKLKCYGIPMLPNTNSTPKYLLVLOGANLK 61  
Db 23 VNTIIYVNGSTTISKYATFLNDRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKK 82  
QY 62 TITLMLRRNNLYVWGSDPENGKCRHYIENDISTERTDYENTLSSSSSRVAMSTINY 121  
Db 83 TITLMLRRNNLYVWGSDPENGKCRHYIENDISTERTDYENTLSSSSSRVAMSTINY 142  
QY 122 SLVPTMEKKAEVNSRNOVOLGIIQLSSDICKISGVDSFPVYTEAFLLVAIQWSEARF 181  
Db 203 KYIENOVKTNNRAFNPPKVINLEETWGIKISTAIHDAKNGVLPKPLELVDAGAKWIVL 262

Db 143 SRYPTELESKAGVKSRSOVOLGIIQLSSDICKISGVDSFPVYTEAFLLVAIQWSEARF 202  
QY 182 KYIENOVKTNNRAFNPPKVINLEEKWKISEAIHNAKNGALPKPLELVDAGKTKWIVL 241  
Db 203 KYIENOVKTNNRAFNPPKVINLEETWGIKISTAIHDAKNGVLPKPLELVDAGAKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
Db 263 RVDEIKPDVALLNIVGGSCOTT 284

Search completed: July 2, 2003, 11:40:28  
Job time: 18.9544 secs



Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYIGPMLPDTNSTPKYLLVKGLOGANLK 61  
DB 1 INTTFDAGNATINKYATFEMESLRNEAKDPSLKCYSIPMLPNTNSTIKYLLVKGLOGASLK 60  
QY 62 TITMLRRNNLYVYGSDPFNGKCRHIFNDITSTPERDVENTLSCSSSSRVASINYN 121  
DB 61 TITMLRRNNLYVYGSDPYD-NKCRHIFNDIKETYSVDVENTLCPSSNPRVAKPINYN 119  
QY 122 SLVPTMEKKAENVSRNOVQGIQLSSDICKISGVDSFPKTEAFELVAIQVSEARF 181  
DB 120 GLYPTLEKAGVTSNEVOLGIISSKIGKISGGSFTKEAEFLVAIQVSEARF 179  
QY 182 KYIENQVKTNFNRAFYDDPKVYNLEEKWKISSEAIHNAKNGALPKPLVDAGTKWIVL 241  
DB 180 KYIENQVKTNFNRPDSNDKVLDEENMGKISTAIHNSKNGALPKPLVDAGTKWIVL 239  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
DB 240 RVDEIKPDVGLLNYVNGTCOAT 261

## RESULT 13

US-08-373-858-2

Sequence 2, Application US/08373858

Patent No. 5633155

GENERAL INFORMATION:

APPLICANT: Kim, Man-Keun

APPLICANT: Lee, Kwan-Ho

APPLICANT: Na, Byeong-Kook

APPLICANT: Jeong, Haeng-Seung

APPLICANT: Choi, Kyu-Wan

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

TITLE OF INVENTION: Expression Vector for Phyto

TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS: Plant Transformed thereof.

ADDRESS: Darby &amp; Darby

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: US

ZIP: 10022-7513

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,858

FILING DATE: 18-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/17986-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7770

TELEFAX: 212-753-6237

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: Protein

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Phyto

Phytolacca americana

TISSUE TYPE: Leaf

US-08-373-858-2

Query Match

Best Local Similarity

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

77.4%; Score 1050; DB 1; Length 313;

76.3%; Pred. No. 5.4e-100;

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYIGPMLPDTNSTPKYLLVKGLOGANLK 61  
DB 23 VNTLIYVNGSTTISKYATFELNDLRNEADPSLKCYSIPMLPNTNSTIKYLLVKGLOGSKK 82  
QY 62 TITMLRRNNLYVYGSDPFNGKCRHIFNDITSTPERDVENTLSCSSSSRVASINYN 121  
DB 83 TITMLRRNNLYVYGSDPFNGKCRHIFNDITSTPERDVENTLSCSSSSRVASINYN 142  
QY 122 SLVPTMEKKAENVSRNOVQGIQLSSDICKISGVDSFPKTEAFELVAIQVSEARF 181  
DB 143 SRPTLESKAGVKSRSOVQGIQLSDINICKISGVMSFTKEAEFLVAIQVSEARF 202  
QY 182 KYIENQVKTNFNRAFYDDPKVYNLEEKWKISSEAIHNAKNGALPKPLVDAGTKWIVL 241  
DB 203 KYIENQVKTNFNRAFYDDPKVYNLEEKWKISSEAIHNAKNGALPKPLVDAGTKWIVL 262  
QY 242 RVDEINRDVALLKYVNGTCOTT 263  
DB 263 RVDEIKPDVALLNYVNGTCOTT 264

## RESULT 14

US-08-500-611-2

Sequence 2, Application US/08500611

Patent No. 5756322

GENERAL INFORMATION:

APPLICANT: Turner, Nilgun E.

TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Lerner, David, Littenberg, Krumholz &amp; Mentlik

STREET: 600 South Avenue West

CITY: Westfield

STATE: NJ

COUNTRY: USA

ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/500,611

FILING DATE: 11-JUL-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REGISTRATION NUMBER: OCIRS 3.0-034

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000

TELEFAX: 908-654-7866

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-500-611-2

Query Match

Best Local Similarity

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;

77.4%; Score 1050; DB 1; Length 313;

76.3%; Pred. No. 5.4e-100;

Matches 200; Conservative 28; Mismatches 34; Indels 0; Gaps 0;



OY 182 KYIENOVKTNNRAFYDDPKVYNLEEKMGKISEAIIHNAKNGALPKPELVDAKGTWIVL 241  
DB 180 KYIENOVKTNNRAFYDDPKVYNLEEKMGKISEAIIHNAKNGALPKPELVDAKGTWIVL 239  
OY 242 RVDEINRDVALLKYVNGTCOTT 263  
DB 240 RVDEIKPDVGLLNVNGTCOAT 261

RESULT 9  
US-07-901-707-9

; Sequence 9, Application US/07901707  
; Patent No. 5376546  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Steve F.  
; APPLICANT: Lane, Julie A.  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/07/901,707  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5376546and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-5750  
; TELETYPE: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-901-707-9

Query Match 80.3%; Score 1089.5; DB 1; Length 261;  
Best Local Similarity 82.4%; Pred. No. 3.6e-104;  
Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

OY 2 INTITFDAGNATINKYATFMESLRNQAADPKLKGICGIMLPDNTSTPYLLVKGLOGANLK 61  
DB 1 INTITFDAGNATINKYATFMESLRNQAADPKLKGICGIMLPDNTSTPYLLVKGLOGANLK 60  
OY 62 TITLMLRRNNLYVWGSDPFGNKKRYHIFNDITSTERTDVENTLCCSSSSRVAMSTNN 121  
DB 61 TITLMLRRNNLYVWGSDPFGNKKRYHIFNDITSTERTDVENTLCCSSSSRVAMSTNN 119  
OY 122 SLVPTMEKKAVNRRNOVAGIOLTLSSDICKISGVDSFPYKTEAFLLVAIOMVSEARF 181  
DB 121 SLVPTMEKKAVNRRNOVAGIOLTLSSDICKISGVDSFPYKTEAFLLVAIOMVSEARF 179

DB 120 GLVPTLEKKAGVTSRNEVOLGIOTLSSICKISGGSFTEIEADFLVAIOMVSEARF 179  
OY 182 KYIENOVKTNNRAFYDDPKVYNLEEKMGKISEAIIHNAKNGALPKPELVDAKGTWIVL 241  
DB 180 KYIENOVKTNNRAFYDDPKVYNLEEKMGKISEAIIHNAKNGALPKPELVDAKGTWIVL 239  
OY 242 RVDEINRDVALLKYVNGTCOTT 263  
DB 240 RVDEIKPDVGLLNVNGTCOAT 261

RESULT 10  
US-07-988-430-9

; Sequence 9, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/07/988,430  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELETYPE: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-988-430-9

Query Match 80.3%; Score 1089.5; DB 1; Length 261;  
Best Local Similarity 82.4%; Pred. No. 3.6e-104;  
Matches 216; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

OY 2 INTITFDAGNATINKYATFMESLRNQAADPKLKGICGIMLPDNTSTPYLLVKGLOGANLK 61  
DB 1 INTITFDAGNATINKYATFMESLRNQAADPKLKGICGIMLPDNTSTPYLLVKGLOGANLK 60  
OY 62 TITLMLRRNNLYVWGSDPFGNKKRYHIFNDITSTERTDVENTLCCSSSSRVAMSTNN 121  
DB 61 TITLMLRRNNLYVWGSDPFGNKKRYHIFNDITSTERTDVENTLCCSSSSRVAMSTNN 119

COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-9

Query Match 80.8%; Score 1096.5; DB 4; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6,8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNOAKDPKLCYGIPLPDTNSTPKYLLVLOGANLK 61  
|||||  
DB 1 INTITFDAGNATINKATFMESLRNEAKDPSLKCVCIPMLPNTNSTIKYLLVLOGASLK 60  
|||||  
QY 62 TITLMLRRNNLYVYGSDPFNGKCRHYHFNIDITSTERDVENTLSSSSSRVAMSINN 121  
|||||  
DB 61 TITLMLRRNNLYVYGSDPYD-NKCRHYHFNIDIKTEYSDEVENTLCPSSNPRVAKPINYN 119  
|||||  
QY 122 SLVPTMEKRAEVNSRNOVOLGIOLSSDICKISGVSPFKTFAFLVAIQVSEARF 181  
|||||  
DB 120 GLVPTLEKKAAGVSRNEVOLGIOLSSDICKISGGSFTKEILEADFLVAIQVSEARF 179  
|||||  
QY 182 KYTENOVKTNFNFAFPDPKVINLEEKMKISEAINHAKGALPKPLELDVTKWIVL 241  
|||||  
DB 180 KYTENOVKTNFNDFSPNDKVIDLEENWGKISTAIHNSKNGALPKPLELNAGTWTIVL 239  
|||||  
QY 242 RVDEINRDVALLKYVNGCQTT 263  
|||||  
DB 240 RVDEIKPDVGLLYVNGTQCAT 261  
|||||

RESULT 8  
US-09-610-838-9  
; Sequence 9, Application US/09610838  
; Patent No. 6376217

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studolka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70, P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-610-838-9

Query Match 80.8%; Score 1096.5; DB 4; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6,8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNOAKDPKLCYGIPLPDTNSTPKYLLVLOGANLK 61  
|||||  
DB 1 INTITFDAGNATINKATFMESLRNEAKDPSLKCVCIPMLPNTNSTIKYLLVLOGASLK 60  
|||||  
QY 62 TITLMLRRNNLYVYGSDPFNGKCRHYHFNIDITSTERDVENTLSSSSSRVAMSINN 121  
|||||  
DB 61 TITLMLRRNNLYVYGSDPYD-NKCRHYHFNIDIKTEYSDEVENTLCPSSNPRVAKPINYN 119  
|||||  
QY 122 SLVPTMEKRAEVNSRNOVOLGIOLSSDICKISGVSPFKTFAFLVAIQVSEARF 181  
|||||  
DB 120 GLVPTLEKKAAGVSRNEVOLGIOLSSDICKISGGSFTKEILEADFLVAIQVSEARF 179  
|||||

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-9

Query Match 80.8%; Score 1096.5; DB 2; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNAKDPKLCYCIPLPPTNSTPKYLVLKLGANLK 61  
DB 1 INTITFDAGNATINKATFMESLRNAKDPKLCYCIPLPPTNSTPKYLVLKLGASLK 60  
QY 62 TTTLMLRRNNLYVMGYSDPFNGKCRHYIFNDITSTERTDVENTLCSSSSRVAMSIYN 121  
DB 61 TTTLMLRRNNLYVMGYSDPYD-NKCRHYIFNDIKGTGYSDVENTLCPSSNPRVAKPIYN 119  
QY 122 SLVPTMEKKAEVNSRQVLOGIQLISSDIGKISGVDSFPVKTAEFFLLVAIOMVSEARF 181  
DB 120 GLVPTLEKKAAGVTSRNEVLOGIQLISSDIGKISGVDSFTEKTEADFLVAIOMVSEARF 179  
QY 182 KYIENQVKTNFNRAFPDPKVINLEEKWKISEAITHNKNKALPKPLVDAKGTWIVL 241  
DB 180 KYIENQVKTNFNRPDSFNDKVLDEENWGKISTAIHNSKNKALPKPLKNAKGTWIVL 239  
QY 242 RVDEINRDVALKLVNGTCQTT 263  
DB 240 RVDEIKPDVGLNLYNGTCQAT 261

## RESULT 6

Sequence 9, Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-9

Query Match 80.8%; Score 1096.5; DB 4; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKATFMESLRNAKDPKLCYCIPLPPTNSTPKYLVLKLGANLK 61  
DB 1 INTITFDAGNATINKATFMESLRNAKDPKLCYCIPLPPTNSTPKYLVLKLGASLK 60  
QY 62 TTTLMLRRNNLYVMGYSDPFNGKCRHYIFNDITSTERTDVENTLCSSSSRVAMSIYN 121  
DB 61 TTTLMLRRNNLYVMGYSDPYD-NKCRHYIFNDIKGTGYSDVENTLCPSSNPRVAKPIYN 119  
QY 122 SLVPTMEKKAEVNSRQVLOGIQLISSDIGKISGVDSFPVKTAEFFLLVAIOMVSEARF 181  
DB 120 GLVPTLEKKAAGVTSRNEVLOGIQLISSDIGKISGVDSFTEKTEADFLVAIOMVSEARF 179  
QY 182 KYIENQVKTNFNRAFPDPKVINLEEKWKISEAITHNKNKALPKPLVDAKGTWIVL 241  
DB 180 KYIENQVKTNFNRPDSFNDKVLDEENWGKISTAIHNSKNKALPKPLKNAKGTWIVL 239  
QY 242 RVDEINRDVALKLVNGTCQTT 263  
DB 240 RVDEIKPDVGLNLYNGTCQAT 261

## RESULT 7

US-09-136-389-9  
Sequence 9, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois

US-08-488-113B-9

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLDPTNSTPKYLLVKGLOGANLK 61  
DB 1 INTTFDAGNATINKYATFMSLRNEAKDPSLCKGIPMLNTNTSTIKYLLVKGLOGASLK 60  
QY 62 TITLMLRRNNLYVMGYSDPFGNKKCRHIFNDITSTERTDVENTLCSSSSRVAMSTYN 121  
DB 61 TITLMLRRNNLYVMGYSDPD-NKCRHYIFNDIKGTESDVNTLCPSSNPRVAKPINYN 119  
QY 122 SLVPTMEKKAENVSRNOVQIGIQLISSDICKISGVDSFPVKTFAFLVATQWSEARF 181  
DB 120 GLYPLEKKAQVTSRNEVQIGIQLISSDICKISGVDSFTEKIEADFLVATQWSEARF 179  
QY 182 KYIENOVKTNFRNFAFPDPKVINLEEKWKISEAIIHNKNGALPKPELVDAKGTWIVL 241  
DB 180 KYIENOVKTNFRNFSPPDKVLDLEENMGKISTAIHNKNGALPKPELVDAKGTWIVL 239  
QY 242 RVDEINRDVALLKYVNGTCQTT 263  
DB 240 RVDEIKPDVGLNLYVNGTCQAT 261

## RESULT 4

US-08-477-484B-9

Sequence 9, Application US/08477484B  
Patent No. 5756699

## GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studix, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-9

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6.8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLDPTNSTPKYLLVKGLOGANLK 61  
DB 1 INTTFDAGNATINKYATFMSLRNEAKDPSLCKGIPMLNTNTSTIKYLLVKGLOGASLK 60  
QY 62 TITLMLRRNNLYVMGYSDPFGNKKCRHIFNDITSTERTDVENTLCSSSSRVAMSTYN 121  
DB 61 TITLMLRRNNLYVMGYSDPD-NKCRHYIFNDIKGTESDVNTLCPSSNPRVAKPINYN 119  
QY 122 SLVPTMEKKAENVSRNOVQIGIQLISSDICKISGVDSFPVKTFAFLVATQWSEARF 181  
DB 120 GLYPLEKKAQVTSRNEVQIGIQLISSDICKISGVDSFTEKIEADFLVATQWSEARF 179  
QY 182 KYIENOVKTNFRNFAFPDPKVINLEEKWKISEAIIHNKNGALPKPELVDAKGTWIVL 241  
DB 180 KYIENOVKTNFRNFSPPDKVLDLEENMGKISTAIHNKNGALPKPELVDAKGTWIVL 239  
QY 242 RVDEINRDVALLKYVNGTCQTT 263  
DB 240 RVDEIKPDVGLNLYVNGTCQAT 261

## RESULT 5

US-08-646-360-9

Sequence 9, Application US/08646360  
Patent No. 5837491

## GENERAL INFORMATION:

APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studix, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

QY 62 TITLMRRNNLYMGYSDFPENGKCRHYHFNIDTSTERTDVENTLCCSSSSRYAMSYNN 121  
Db 61 TITLMRRNNLYMGYSDFPD-NKCRHYHFNIDKGTESYDVENTLCPSSNPRVAKPINYN 119  
QY 122 SLVPTMEKKAEVSRNOVOGLIOILSSDGIKISGVDSFPVKTEAFLLVAIOMVSEARF 181  
Db 120 GLVPTLEKKAAGVSRNEVOGLIOILSSDGIKISGVDSFTEKIEAKFLVAIOMVSEARF 179  
QY 182 KYIENOVKTNFNAFYPPDPKVINLEEKMGKISEAIHNAKNGALPKPLELVDAKGTWIVL 241  
Db 180 KYIENOVKTNFNRDPSFNKVDLDEENMGKISTAHNSKNGALPKPLELVDAKGTWIVL 239  
QY 242 RVDEINRDVALLKYVNGTCQT 263  
Db 240 RVDEIKPDVGLLVNGTCQAT 261

RESULT 2  
US-08-485-286-79

; Sequence 79, Application US/08485286  
; Patent No. 5646026  
; Patent No. 5646026 5646119  
; GENERAL INFORMATION:  
; APPLICANT: WALSH, TERENCE A  
; APPLICANT: HEY, TIMOTHY D  
; APPLICANT: MORGAN, ALICE ER  
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ANDREA T. BORUCKI  
; STREET: 9330 ZIONSVILLE ROAD  
; CITY: INDIANAPOLIS  
; STATE: IN  
; COUNTRY: US  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,286  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378761  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BORUCKI, ANDREA T  
; REGISTRATION NUMBER: 33651  
; REFERENCE/DOCKET NUMBER: 38272B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317) 337-4846  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-485-286-79

Query Match 80.8%; Score 1096.5; DB 1; Length 261;  
Best Local Similarity 82.8%; Pred. No. 6,8e-105;  
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;

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Db 1 INTITFDAGNATINKYATFMESLRNKAQDPKSLKCGIRPLPTNSTITLLVKGLOGASLK 60

QY 62 TITLMRRNNLYMGYSDFPENGKCRHYHFNIDTSTERTDVENTLCCSSSSRYAMSYNN 121  
Db 61 TITLMRRNNLYMGYSDFPD-NKCRHYHFNIDKGTESYDVENTLCPSSNPRVAKPINYN 119  
QY 122 SLVPTMEKKAEVSRNOVOGLIOILSSDGIKISGVDSFPVKTEAFLLVAIOMVSEARF 181  
Db 120 GLVPTLEKKAAGVSRNEVOGLIOILSSDGIKISGVDSFTEKIEAKFLVAIOMVSEARF 179  
QY 182 KYIENOVKTNFNAFYPPDPKVINLEEKMGKISEAIHNAKNGALPKPLELVDAKGTWIVL 241  
Db 180 KYIENOVKTNFNRDPSFNKVDLDEENMGKISTAHNSKNGALPKPLELVDAKGTWIVL 239  
QY 242 RVDEINRDVALLKYVNGTCQT 263  
Db 240 RVDEIKPDVGLLVNGTCQAT 261

RESULT 3  
US-08-486-113B-9

; Sequence 9, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/9988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

GenCore version 5.1.6  
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OM:protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 16.9544 Seconds  
(without alignments)  
456,414 Million cell updates/sec

Title: US-09-978-274A-4  
Perfect score: 1357  
Sequence: 1 MINTIFDGNATINKYATF.....DEINRDVALLKYVNGTCQT 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/1aa/5D\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/5E\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/5F\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096.5	80.8	261	1 US-08-378-761A-79	Sequence 79, Appl
2	1096.5	80.8	261	1 US-08-485-286-79	Sequence 79, Appl
3	1096.5	80.8	261	1 US-08-488-113B-9	Sequence 9, Appl
4	1096.5	80.8	261	1 US-08-477-484B-9	Sequence 9, Appl
5	1096.5	80.8	261	2 US-08-646-360-9	Sequence 9, Appl
6	1096.5	80.8	261	4 US-08-839-765-9	Sequence 9, Appl
7	1096.5	80.8	261	4 US-09-136-389-9	Sequence 9, Appl
8	1096.5	80.8	261	4 US-09-610-838-9	Sequence 9, Appl
9	1089.5	80.3	261	1 US-07-901-707-9	Sequence 9, Appl
10	1089.5	80.3	261	1 US-07-988-430-9	Sequence 9, Appl
11	1089.5	80.3	261	1 US-08-425-336-9	Sequence 9, Appl
12	1089.5	80.3	261	5 PCT-US92-09487-9	Sequence 9, Appl
13	1050	77.4	313	1 US-08-373-858-2	Sequence 2, Appl
14	1050	77.4	313	1 US-08-500-611-2	Sequence 2, Appl
15	1050	77.4	313	2 US-08-500-694-2	Sequence 2, Appl
16	1050	77.4	313	4 US-09-005-273-2	Sequence 2, Appl
17	1050	77.4	313	5 PCT-US96-11546-2	Sequence 2, Appl
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19	1042	76.8	313	4 US-09-005-273-4	Sequence 4, Appl
20	862.5	63.6	305	1 US-08-138-636-2	Sequence 2, Appl
21	862.5	63.6	305	1 US-08-319-622A-2	Sequence 2, Appl
22	862.5	63.6	305	1 US-08-471-564-2	Sequence 2, Appl
23	342	25.2	259	1 US-07-901-707-10	Sequence 10, Appl
24	342	25.2	259	1 US-07-988-430-10	Sequence 10, Appl
25	342	25.2	259	1 US-08-425-336-10	Sequence 10, Appl
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28	342	25.2	259	2 US-08-646-360-10	Sequence 10, Appl
29	342	25.2	259	4 US-08-839-765-10	Sequence 10, Appl
30	342	25.2	259	4 US-09-136-389-10	Sequence 10, Appl
31	342	25.2	259	4 US-09-610-838-10	Sequence 10, Appl
32	342	25.2	259	5 PCT-US92-09487-10	Sequence 10, Appl
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36	319.5	23.5	292	1 US-08-378-761A-81	Sequence 81, Appl
37	319.5	23.5	292	1 US-08-465-286-81	Sequence 81, Appl
38	316	23.3	251	1 US-08-425-336-108	Sequence 108, App
39	316	23.3	251	1 US-08-488-113B-108	Sequence 108, App
40	316	23.3	251	1 US-08-477-484B-108	Sequence 108, App
41	316	23.3	251	2 US-08-646-360-108	Sequence 108, App
42	316	23.3	251	4 US-08-839-765-108	Sequence 108, App
43	316	23.3	251	4 US-09-136-389-108	Sequence 108, App
44	316	23.3	251	4 US-09-610-838-108	Sequence 108, App
45	314	23.1	251	1 US-08-425-336-101	Sequence 101, App

## ALIGNMENTS

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RESULT 1
US-08-378-761A-79
: Sequence 79, Application US/08378761A
: Patent No. 5635384
:
: GENERAL INFORMATION:
: APPLICANT: WALSH, TERENCE A
: APPLICANT: HEY, TIMOTHY D
: APPLICANT: MORGAN, ALICE ER
: TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
: TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ANDREA T. BORUCKI
: STREET: 9330 ZIONSVILLE ROAD
: CITY: INDIANAPOLIS
: STATE: IN
: COUNTRY: US
: ZIP: 46268
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/378,761A
: FILING DATE: 26-JAN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BORUCKI, ANDREA T
: REGISTRATION NUMBER: 33651
: REFERENCE/DOCKET NUMBER: 38272B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (317) 337-4846
: INFORMATION FOR SEQ ID NO: 79:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 261 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-378-761A-79

Query Match      80.8%; Score 1096.5; DB 1; Length 261;
Best Local Similarity 82.8%; Pred. No. 6.8e-105;
Matches 217; Conservative 14; Mismatches 30; Indels 1; Gaps 1;
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|||||
1 INTTFPAGNATINKYATFMESLRNKAADKSLACYGIPMLPDTNSTIKYLLVLOGASLK 60
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Db 189 AHDAKNGVLPKPLELVDSAGAKWIVLRVDEIKPDVALLNYYGSGSCOTT 237

Search completed: July 2, 2003, 11:39:42  
Job time : 21.0629 secs



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Best Local Similarity 82.6%. Pred. No. 1.2e-46; Indels 0; Gaps 0;
Matches 90; Conservative 5; Mismatches 14;
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DB 125 GWSFETKTEAEFFLLVAIQMWSEARAFKYYINQVKTNNRAFFNPNPKYLNLEETMGKIST 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 62 AIHNAKNGALPKPLEVDAKGTKNIVLRVDEINRDVALLKYVNGTCQTT 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 185 AIHADKNGVLPKPLEVDASGAKWIVLRVDEIKPDVALLNVGSCQTT 233
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
AAW14245
ID AAW14245 standard; protein: 234 AA.
XX
AC AAW14245;
XX
DT 25-JUN-1997 (first entry)
XX
DE Mature pokeweed antiviral protein deletion variant (29-262).
XX
KM Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KM stem-loop; 26S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KM translation; broad spectrum; resistance; cell death; sterility; nematode;
KM bacterium.
XX
OS Phytolacca americana.
XX
MN W09703183-A1.
XX
PD 30-JAN-1997.
XX
PE 11-JUL-1996; 96MO-US11546.
XX
PR 11-JUL-1995; 95US-0500694.
XX
PA 11-JUL-1995; 95US-0500611.
XX
(PUTF ) UNIV Rutgers STATE NEW JERSEY.
XX
PI Turner NE;
XX
DR WPI: 1997-119040/11.
XX
PT New pokeweed antiviral protein mutants - which exhibit anti-viral
PT and anti-fungal activity in plants and have reduced phytotoxicity
PS Claim 14; -: 64pp: English.
XX
Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
mutants having reduced phytotoxicity but retaining anti-viral or
anti-fungal activity in plants. The sequences' numbering corresponds to
the 262 amino acid mature protein. The proteins AAW14165-W14217
represent serial deletions from the C-terminus whereas sequences
AAW14218-55 are serial deletions from the N-terminus. Prior to
processing, the protein contains a 22 amino acid N-terminal signal
sequence and a 29 amino acid C-terminal extension. PAP is a Type I
ribosomal inhibitor protein (RIP) that catalyses the removal of a
specific adenine residue from a highly conserved stem-loop structure in
the 26S rRNA of eukaryotic ribosomes and also interferes with elongation
factor-2 binding thus blocking protein translation. The PAP mutants can
confer broad spectrum virus and fungus resistance to plants without
causing plant cell death or sterility. They can also confer increased
resistance to insects, bacteria and nematodes in plants.
CC N.B. This sequence is not given in the specification but is generated
CC from the wild type sequence reproduced in the specification.
CC
SQ Sequence 234 AA:
Query Match 79.8%; Score 454; DB 18; Length 234;
Best Local Similarity 82.6%; Pred. No. 1.2e-46;
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

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QY      2 GVDSPPVTEAFLLVAIQMWSEARFYIENQVKTNNRAFYDDPKVYNLEEKMGKISE 61
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      126 GVMSTETKEAEFLFLVAIQMWSEARFYIENQVKTNNRAFYDDPKVYNLEEKMGKIST 185
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY      62 AIHNAKNALPKPELVDAKGTQKIVLVDENRDLAKTKVNGSCQTT 110
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      186 AIHDAKNVLPKPELVDAKGTQKIVLVDENRDLAKTKVNGSCQTT 234
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 13
AAW14244
AAW14244 standard; protein: 235 AA.
XX
AC AAW14244;
XX
DT 25-JUN-1997 (first entry)
XX
DE Mature pokeweed antiviral protein deletion variant (28-262).
XX
KW Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;
KW translocation; broad spectrum; resistance; cell death; sterility; nematode;
KW bacterium.
XX
OS Phytolacca americana.
XX
PN W09703183-A1.
XX
PD 30-JAN-1997.
XX
PF 11-JUL-1996; 96MO-US11546.
XX
PR 11-JUL-1995; 95US-0500694.
PR 11-JUL-1995; 95US-0500611.
XX
PA (RUPF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Turner NE;
XX
DR WPI; 1997-119040/11.
XX
XX New pokeweed antiviral protein mutants - which exhibit anti-viral
PT and anti-fungal activity in plants and have reduced phytotoxicity
XX
XX Claim 14; -: 64BP: English.
XX
PS
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)
CC mutants having reduced phytotoxicity but retaining anti-viral or
CC anti-fungal activity in plants. The sequences' numbering corresponds to
CC the 262 amino acid mature protein. The proteins AAW14163-W14217
CC represent serial deletions from the C-terminus whereas sequences
CC AAW14218-55 are serial deletions from the N-terminus. Prior to
CC processing, the protein contains a 22 amino acid N-terminal signal
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a
CC specific adenine residue from a highly conserved stem-loop structure in
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation
CC factor-2 binding thus blocking protein translation. The PAP mutants can
CC confer broad spectrum virus and fungus resistance to plants without
CC causing plant cell death or sterility. They can also confer increased
CC resistance to insects, bacteria and nematodes in plants.
CC N.B. This sequence is not given in the specification but is generated
CC from the wild type sequence reproduced in the specification.
XX
SQ Sequence 235 AA;

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XX Sequence 231 AA;  
SO Query Match 79.8%; Score 454; DB 18; Length 231;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSFPKTEAFLLVAIQWSEARFKYIENOVKTFNRAFPDPKVINLEEKWKISE 61  
DB 123 GWSFTEKTEAFLLVAIQWSEARFKYIENOVKTFNRAFPDPKVINLEETWKIST 182  
OY 62 AIHAKKAGLPKPELVDAKGTKWIVLRVDIENDVALLKRVNGTCOTT 110  
DB 183 AIHDAKNGVLPKPELVDAKGAKWIVLRVDIENKPDVALLNVGSCOTT 231

RESULT 10  
AAW14247  
ID AAW14247 standard; protein: 232 AA.  
AC AAW14247;  
XX 25-JUN-1997 (first entry)  
DT  
XX Mature pokeweed antiviral protein deletion variant (31-262).  
DE  
XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
KM  
XX Phytoacca americana.  
OS  
XX W09703183-A1.  
PN  
XX 30-JAN-1997.  
PD  
XX 11-JUL-1996; 96WO-US11546.  
PF  
XX 11-JUL-1995; 95US-0500694.  
PR 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PA  
XX Tuner NE;  
PI  
XX WPI: 1997-119040/11.  
DR  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytoxicity  
XX  
XX Claim 14: -: 64pp; English.  
PS  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW1418-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SO Sequence 232 AA;

XX Query Match 79.8%; Score 454; DB 18; Length 232;  
SO Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSFPKTEAFLLVAIQWSEARFKYIENOVKTFNRAFPDPKVINLEEKWKISE 61  
DB 124 GWSFTEKTEAFLLVAIQWSEARFKYIENOVKTFNRAFPDPKVINLEETWKIST 183  
OY 62 AIHAKKAGLPKPELVDAKGTKWIVLRVDIENDVALLKRVNGTCOTT 110  
DB 184 AIHDAKNGVLPKPELVDAKGAKWIVLRVDIENKPDVALLNVGSCOTT 232

RESULT 11  
AAW14246  
ID AAW14246 standard; protein: 233 AA.  
AC AAW14246;  
XX 25-JUN-1997 (first entry)  
DT  
XX Mature pokeweed antiviral protein deletion variant (30-262).  
DE  
XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.  
KM  
XX Phytoacca americana.  
OS  
XX W09703183-A1.  
PN  
XX 30-JAN-1997.  
PD  
XX 11-JUL-1996; 96WO-US11546.  
PF  
XX 11-JUL-1995; 95US-0500694.  
PR 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
PA  
XX Tuner NE;  
PI  
XX WPI: 1997-119040/11.  
DR  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytoxicity  
XX  
XX Claim 14: -: 64pp; English.  
PS  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW1418-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
SO Query Match 233 AA; 79.8%; Score 454; DB 18; Length 233;





CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

XX Sequence 225 AA:

Query Match 79.8%; Score 454; DB 18; Length 225;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSEPVKTEAFLLVAIQWSEARFKYIENQVKTNFRAPYPPKVINLEKKGKIS 61  
DB 117 GVMSTKTEAFLLVAIQWSEARFKYIENQVKTNFRAPYPPKVINLEKKGKIS 176  
OY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKVNGTCQTT 110  
DB 177 AIHDAKNGVLPKPELVDAKGTWIVLRVDEINRDVALLKVNGTCQTT 225

RESULT 4

AAW14253 standard; protein: 226 AA.

XX AAW14253;

DT 25-JUN-1997 (first entry)

XX Mature pokeweed antiviral protein deletion variant (37-262).

XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.

OS Phytolacca americana.

PN W09703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
XX and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14: -; 64pp: English.

XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal

CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.

XX Sequence 226 AA:

Query Match 79.8%; Score 454; DB 18; Length 226;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 GVDSEPVKTEAFLLVAIQWSEARFKYIENQVKTNFRAPYPPKVINLEKKGKIS 61  
DB 118 GVMSTKTEAFLLVAIQWSEARFKYIENQVKTNFRAPYPPKVINLEKKGKIS 177  
OY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALLKVNGTCQTT 110  
DB 178 AIHDAKNGVLPKPELVDAKGTWIVLRVDEINRDVALLKVNGTCQTT 226

RESULT 5

AAW14252 standard; protein: 227 AA.

XX AAW14252;

DT 25-JUN-1997 (first entry)

XX Mature pokeweed antiviral protein deletion variant (36-262).

XX Pokeweed antiviral protein; mutant; phytoxicity; anti-viral; virus;  
KW anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KW stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KW translation; broad spectrum; resistance; cell death; sterility; nematode;  
KW bacterium.

OS Phytolacca americana.

PN W09703183-A1.

PD 30-JAN-1997.

PF 11-JUL-1996; 96WO-US11546.

PR 11-JUL-1995; 95US-0500694.

PR 11-JUL-1995; 95US-0500611.

PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Turner NE;

DR WPI: 1997-119040/11.

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
XX and anti-fungal activity in plants and have reduced phytoxicity

PS Claim 14: -; 64pp: English.

XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyzes the removal of a

XX New pokeweed antiviral protein (PAP) with similar activity to  
PT ricin - used to treat cancer and as an agricultural chemical  
XX  
XX Claim 1: Page 11-13; 14pp: Japanese.  
XX  
XX NB: A protein comprising 261 amino acids is claimed.  
CC PAP has a similar activity to ricin, i.e. inhibits protein synthesis.  
CC The protein may be obtained all year round by recombinant DNA  
CC techniques. PAP can be used partic. against cancer and as an  
CC agricultural chemical.  
CC Total mRNA, is extracted from the seeds, leaves and roots of  
CC pokeweed and used to prepare cDNA using PCR. The resultant cDNA is  
CC used to prepare two DNA fractions, which are introduced into a  
CC cloning vector EMBL3 and then into host E.coli PLX-17 (P2) to  
CC produce PAP.  
XX  
XX Sequence 294 AA:  
SQ  
Query Match 80.3%; Score 457; DB 14; Length 294;  
Best Local Similarity 82.6%; Pred. No. 7.3e-47;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
OY 2 GVDSPFKTEAFPLVAIQWSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 61  
DB 177 GVDSPFKTEAFPLVAIQWSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 236  
OY 62 AIHNAKNGALPKRLELDVDAKGTWKIYLRVDEINRDVALLKYVNGCOTT 110  
DB 237 AIHNAKNGALTPLELKNANGSKWIVLRVDIEPDVGLKYVNGCOTAT 285

RESULT 2  
AAW14255  
ID AAW14255 standard; protein: 224 AA.  
XX  
AC AAW14255;  
XX  
DT 25-JUN-1997 (first entry)  
XX  
DE Mature pokeweed antiviral protein deletion variant (39-262).  
XX  
XX Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;  
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
KM bacterium.  
XX  
XX Phytolacca americana.  
XX  
OS  
XX  
PN MO9703183-A1.  
XX  
PD 30-JAN-1997.  
XX  
PF 11-JUL-1996; 96WO-US11546.  
XX  
PR 11-JUL-1995; 95US-0500694.  
XX  
PR 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Turner NE;  
XX  
DR WPI: 1997-119040/11.  
XX  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
XX Claim 14: -: 64pp; English.  
XX  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC anti-fungal activity in plants. The sequences' numbering corresponds to

CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences  
CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
CC processing, the protein contains a 22 amino acid N-terminal signal  
CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
CC specific adenine residue from a highly conserved stem-loop structure in  
CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
CC factor-2 binding thus blocking protein translation. The PAP mutants can  
CC confer broad spectrum virus and fungus resistance to plants without  
CC causing plant cell death or sterility. They can also confer increased  
CC resistance to insects, bacteria and nematodes in plants.  
CC N.B. This sequence is not given in the specification but is generated  
CC from the wild type sequence reproduced in the specification.  
XX  
XX Sequence 224 AA:  
SQ  
Query Match 79.8%; Score 454; DB 18; Length 224;  
Best Local Similarity 82.6%; Pred. No. 1.2e-46;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
OY 2 GVDSPFKTEAFPLVAIQWSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 61  
DB 116 GVDSPFKTEAFPLVAIQWSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 175  
OY 62 AIHNAKNGALPKRLELDVDAKGTWKIYLRVDEINRDVALLKYVNGCOTT 110  
DB 176 AIHDAKNGVLPKRLELDVDAKGTWKIYLRVDEINRDVALLKYVNGSCOTT 224

RESULT 3  
AAW14254  
ID AAW14254 standard; protein: 225 AA.  
XX  
AC AAW14254;  
XX  
DT 25-JUN-1997 (first entry)  
XX  
DE Mature pokeweed antiviral protein deletion variant (38-262).  
XX  
XX Pokeweed antiviral protein; mutant; phytotoxicity; anti-viral; virus;  
KM anti-fungal; fungus; plant; ribosomal inhibitor protein; adenine; insect;  
KM stem-loop; 28S rRNA; eukaryotic; ribosome; elongation factor-2 binding;  
KM translation; broad spectrum; resistance; cell death; sterility; nematode;  
KM bacterium.  
XX  
XX Phytolacca americana.  
XX  
OS  
XX  
PN MO9703183-A1.  
XX  
PD 30-JAN-1997.  
XX  
PF 11-JUL-1996; 96WO-US11546.  
XX  
PR 11-JUL-1995; 95US-0500694.  
XX  
PR 11-JUL-1995; 95US-0500611.  
XX  
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
XX  
PI Turner NE;  
XX  
DR WPI: 1997-119040/11.  
XX  
XX New pokeweed antiviral protein mutants - which exhibit anti-viral  
PT and anti-fungal activity in plants and have reduced phytotoxicity  
XX  
XX Claim 14: -: 64pp; English.  
XX  
XX Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
CC mutants having reduced phytotoxicity but retaining anti-viral or  
CC anti-fungal activity in plants. The sequences' numbering corresponds to  
CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
CC represent serial deletions from the C-terminus whereas sequences





DB 85 -GTVSLGLARVNLVVAFAVNDNRNVNRAVYFRFEINSAELRTVPEVTVANQ-----R 137  
 QY 117 SINNSLYPTMEKKAEV---NSRNQVQLGIQLSSDIGKIS 154  
 DB 138 PLEYTEDYQSIEKNKAKITTGDKSRKRELGLIDLLISTIDKVN 179

## RESULT 14

Q93Y65 PRELIMINARY: PRT: 294 AA.

AC 093Y65;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DE RNA -glycosidase (EC 3.2.2.22).  
 OS Dianthus chinensis.  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.  
 OX NCBI\_TaxID=118431;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20306826; Pubmed=10850653;  
 RA Cho H.J., Lee S.J., Kim S., Kim B.D.;  
 RT "Isolation and characterization of cDNAs encoding ribosome  
 inactivating protein from Dianthus sinensis L.";  
 RL Mol. Cells 10:135-141(2000).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF219237; AAK68928.1; -;  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR Hydrolyase; Toxin.  
 KW Hydrolyase; Toxin.  
 SQ SEQUENCE 294 AA: 33331 MM: 659E72DD847A72D0 CRC64:

Query Match 22.3%, Score 177; DB 10; Length 294;  
 Best Local Similarity 31.5%, Pred. No. 3.6e-09;  
 Matches 51; Conservative 30; Mismatches 65; Indels 16; Gaps 6;

QY 2 INTITPDGNAITINKVATFMSLNRQAQDKPKLCYG--IPMLPDTNSTPKYLLVKLOGAN 59  
 DB 25 VRTITLDIARTPAKYSFSDQIRNNMMDPRLKYCSTEIAVAKPSVADKFLRINFQGR 84  
 QY 60 LKTTTLMRLNNLLVMGYSDPFNGNKR-YHIFNDITSTERTDV--ENTLCSSSSSRYAM 116  
 DB 85 -GTVSLGLARVNLVVAFAVNDNRNVNRAVYFRFEINSAELRTVPEVTVANQ-----R 137  
 QY 117 SINNSLYPTMEKKAEV---NSRNQVQLGIQLSSDIGKIS 154  
 DB 138 PLEYTEDYQSIEKNKAKITTGDKSRKRELGLIDLLISTIDKVN 179

## RESULT 15

Q93Y64 PRELIMINARY: PRT: 294 AA.

AC 093Y64;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DE RNA -glycosidase (EC 3.2.2.22).  
 OS Dianthus chinensis.  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.  
 OX NCBI\_TaxID=118431;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20306826; Pubmed=10850653;  
 RA Cho H.J., Lee S.J., Kim S., Kim B.D.;  
 RT "Isolation and characterization of cDNAs encoding ribosome  
 inactivating protein from Dianthus sinensis L.";

RL Mol. Cells 10:135-141(2000).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF219238; AAK68929.1; -;  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR Hydrolyase; Toxin.  
 KW Hydrolyase; Toxin.  
 SQ SEQUENCE 294 AA: 33267 MM: E196CE3F1DF97C82 CRC64:

Query Match 22.3%, Score 177; DB 10; Length 294;  
 Best Local Similarity 31.5%, Pred. No. 3.6e-09;  
 Matches 51; Conservative 30; Mismatches 65; Indels 16; Gaps 6;

QY 2 INTITPDGNAITINKVATFMSLNRQAQDKPKLCYG--IPMLPDTNSTPKYLLVKLOGAN 59  
 DB 25 VRTITLDIARTPAKYSFSDQIRNNMMDPRLKYCSTEIAVAKPSVADKFLRINFQGR 84  
 QY 60 LKTTTLMRLNNLLVMGYSDPFNGNKR-YHIFNDITSTERTDV--ENTLCSSSSSRYAM 116  
 DB 85 -GTVSLGLARVNLVVAFAVNDNRNVNRAVYFRFEINSAELRTVPEVTVANQ-----R 137  
 QY 117 SINNSLYPTMEKKAEV---NSRNQVQLGIQLSSDIGKIS 154  
 DB 138 PLEYTEDYQSIEKNKAKITTGDKSRKRELGLIDLLISTIDKVN 179

Search completed: July 2, 2003, 11:42:10  
 Job time : 23.2767 secs

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Db 26 VTFDLETASKTKYGTFTSLNLRNIVKDSKLYEGIPMLPAPIKAPAKYLLAEKAKAGTDI 85
Oy 61 KTTTLMRLRNLLYVMGSDPFNGNKKCRHYHFNIDITERTDVENTLSSSSSRVAMSLNY 120
Db 86 -TTTAAVSKNDLYVAFTDVOAG-KLRAHFDPDISLATAKAIFPT-----ATGYIOIGY 137
Oy 121 NSLYPTMEKKAENSRNOVOLG 142
Db 138 TSNVYSIEGAAGSN-RVNFOLG 158

RESULT 11
O9M5K6 PRELIMINARY: PRT: 279 AA.
AC O9M5K6:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE rRNA-glycosidase (EC 3.2.2.22).
GN CAP30A.
OS Chenopodium album (Lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
NCBI_TaxID=3559;
RN
RP SEQUENCE FROM N.A.
RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;
RT "A cDNA clone encoding a novel ribosome inactivating protein from
RT Chenopodium album L.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF228508; AAF66234.1;
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHGARICIN.
DR HydroLase: Toxin.
KW SEQUENCE 279 AA; 31377 MW; 2A53300E445DC952 CRC64;

Query Match 24.2%; Score 192; DB 10; Length 279;
Best Local Similarity 36.8%; Pred. No. 1.2e-10;
Matches 53; Conservative 20; Mismatches 63; Indels 8; Gaps 5;

Oy 13 TINKYATFMSLRNOAKDPKLCYGIPLDPDNTSPRYLVKLOGA---NKTTTLMRLR 69
Db 37 TONTYNTFMSLRNOAKDPKLCYGIPLDPDNTSPRYLVKLOGA---NKTTTLMRLR 96
Oy 70 NNLVYMGSDPFNGNKKCRHYHFNIDITERTDVENTLSSSSSRVAMSLNYPTMEK 129
Db 97 NDLVVAAYADKF-GGKVRGHYFKNL-GISTIDEANKYFPNVQDFI--NITYGESYNOIES 152
Oy 130 KAEVNSRNOVOLGIQILSSDICKI 153
Db 153 NAGTN-RLSPFLGFDLTKISRNKV 175

RESULT 12
O9AUE3 PRELIMINARY: PRT: 279 AA.
AC O9AUE3:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE rRNA-glycosidase (EC 3.2.2.22).
GN CAP30B.
OS Chenopodium album (Lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
NCBI_TaxID=3559;

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RN [1]
RP SEQUENCE FROM N.A.
RA Park J.S., Lee S.M., Kim Y.T., Cho K.J.;
RT "Molecular characterization of a new cDNA clone encoding a ribosome-
RT inactivating protein (CAP30B) from Chenopodium album.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF230812; AAK28323.1;
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHGARICIN.
KW HydroLase: Toxin.
KW SEQUENCE 279 AA; 31419 MW; 97E934F22C8033AF CRC64;

Query Match 23.7%; Score 188; DB 10; Length 279;
Best Local Similarity 36.6%; Pred. No. 2.9e-10;
Matches 53; Conservative 23; Mismatches 59; Indels 10; Gaps 5;

Oy 13 TINKYATFMSLRNOAKDPKLCYGIPLDPDNTSPRYLVKLOGA---NKTTTLMRLR 69
Db 37 TONTYNTFMSLRNOAKDPKLCYGIPLDPDNTSPRYLVKLOGA---NKTTTLMRLR 96
Oy 70 NNLVYMGSDPFNGNKKCRHYHFNIDITERTDVENTLSSSSSRVAMSLNYPTME 128
Db 97 NDLVVAAYADKF-GGKVRGHYFKNLGIST---IDKAKKYFPNVQDFINITYGESYNOIE 151
Oy 129 KAEVNSRNOVOLGIQILSSDICKI 153
Db 152 NAGTN-RLSPFLGFDLTKITNKV 175

RESULT 13
O93Y66 PRELIMINARY: PRT: 294 AA.
AC O93Y66:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE rRNA-glycosidase (EC 3.2.2.22).
GN RiP1.
OS Dianthus chinensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Dianthus.
NCBI_TaxID=118431;
RN
RP SEQUENCE FROM N.A.
RA MEDLINE-20306826; PubMed-10850653;
RA Cho H.J., Lee S.J., Kim S., Kim B.D.;
RT "Isolation and characterization of cDNAs encoding ribosome
RT inactivating protein from Dianthus sinensis L.";
RL Mol. Cells 10:135-141(2000).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF219236; AAK68927.1;
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR HydroLase: Toxin.
KW SEQUENCE 294 AA; 33369 MW; 927D93C494EF6C95 CRC64;

Query Match 22.7%; Score 180; DB 10; Length 294;
Best Local Similarity 32.1%; Pred. No. 1.9e-09;
Matches 52; Conservative 29; Mismatches 65; Indels 16; Gaps 6;

Oy 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGIPLDPDNTSPRYLVKLOGAN 59
Db 25 VTFETDLAPRTAKKSSFLDQIRNNMRDPLKCYGSEIVAVIAKPVADKFLRINFGPR 84
Oy 60 LKTTTLMRLRNLLYVMGSDPFNGNKKCR-YHFNIDITERTDVT--ENTLSSSSSRVAM 116

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DE rRNA -glycosidase (EC 3.2.2.22).
GN RIP.
OS Clorodendrum aculeatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Clorodendrum.
OX NCBI_TaxID=54208;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF.
RX MEDLINE=97238481; PubMed=9132066;
RA Kumar D., Verma H.N., Tuteja N., Tewari K.K.;
RT "Cloning and characterization of a gene encoding an antiviral protein
RT from Clorodendrum aculeatum L."
RL Plant Mol. Biol. 33:745-751(1997).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: X96474; CAA65328.1; -.
DR EMBL: X96583; CAA65402.1; -.
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KM Glycosidase; Hydrolase; Toxin.
SQ SEQUENCE 302 AA; 33955 MW; B0561C3918C2E6A2 CRC64;

Query Match 50.3%; Score 399; DB 10; Length 302;
Best Local Similarity 54.1%; Pred. No. 1,2e-30;
Matches 80; Conservative 20; Mismatches 46; Indels 2; Gaps 2;

OY 7 PDAGNATINKYATFMESLRNOKADPKLCYGIPLMDTSTPKYLLVKGANLKTITLM 66
DB 30 FHWGATITITFTFTFLTEAADAASLRKCYGLPMLPTTQPKHVLRLDADATTITLI 89
OY 67 LRRNNLYVYGSDPFNGNRCRYHIFNDITSTERTDVENTLSCSSSRVAMSIYNLSLYPT 126
DB 90 YNRTNLVYLGSDPFNG-ECRYHIFSDVAGTDRTEAVTLCPDRENRVQKDIWFESNYQS 148
OY 127 MEKKAEVNSRNOVQGIQILSSDIGIS 154
DB 149 MENKAG-KSRAQLELGINILKSIKIS 175
DB

RESULT 9
P93261 PRELIMINARY; PRT: 289 AA.
ID P93261;
AC P93261;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE rRNA -glycosidase (EC 3.2.2.22).
GN RIP.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_TaxID=544;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98087998; PubMed=9426592;
RA Rippmann J.F., Michalowski C.B., Nelson D.E., Bohnert H.J.;
RT "Induction of a ribosome-inactivating protein upon environmental
RT stress."
RL Plant Mol. Biol. 35:701-709(1997).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: U80072; AAB96824.1; -.
DR HSSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.

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DR PRINTS: PR00396; SHIGARICIN.
KM Glycosidase; Hydrolase; Toxin.
SQ SEQUENCE 289 AA; 32652 MW; 132AA996FA27F1D CRC64;

Query Match 35.1%; Score 278.5; DB 10; Length 289;
Best Local Similarity 39.3%; Pred. No. 5,3e-19;
Matches 59; Conservative 28; Mismatches 62; Indels 1; Gaps 1;

OY 4 TTFDAGNATINKYATFMESLRNOKADPKLCYGIPLMDTSTPKYLLVKGANLKTIT 63
DB 23 TLVLIDGATKTEKTYSDPMKRLTEAGKDPNRYVGLSMKPKPKPPYLLVLELVKSDMSI 82
OY 64 TMLRRNNLYVYGSDPFNGNRCRYHIFNDITSTERTDVENTLSCSSSRVAMSIYNLS 123
DB 83 TILSLRNDLYVYGSDPMYNG-KCRYHVFDPDHSKRPYQHSCLKAKADAIKPKIGYSS 141
OY 124 YPTMEKKAEVNSRNOVQGIQILSSDIGI 153
DB 142 YTEIERKAKVRNRKEIGLVNKLKTLIPKV 171
DB

RESULT 10
Q39418 PRELIMINARY; PRT: 272 AA.
ID Q39418;
AC Q39418;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Antiviral protein precursor (Ribosome-inactivating protein) (RNA N-
DE glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)
DE (BETAVULGIN) (BVG).
GN RIP OR BETAVULGIN OR BVG.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=3555;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=SEEDLING.
RX MEDLINE=96235141; PubMed=8666251;
RA Horning E., Wajant H., Jeske H., Mundy K.-W.;
RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from
RT Beta vulgaris vulgaris (mangold)".
RL Gene 170:233-236(1996).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN
CC SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR
CC SUICIDE UPON INVASION BY A VIRUS.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
CC PROTEINS.
CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.
DR EMBL: X85967; CAA59952.1; -.
DR HSSP: O03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; FALSE_NEG.
KM Hydrolyase; Glycosidase; Antiviral; Protein synthesis inhibitor; Toxin;
KM Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 272 BY SIMILARITY.
FT ACT_SITE 196 196 ANTIYIRAL PROTEIN.
FT ACT_SITE 272 272 BY SIMILARITY.
SQ SEQUENCE 272 AA; 30168 MW; 77DD0917FD12EDFF CRC64;

Query Match 24.3%; Score 192.5; DB 10; Length 272;
Best Local Similarity 38.7%; Pred. No. 1e-10;
Matches 55; Conservative 20; Mismatches 54; Indels 13; Gaps 5;

OY 5 ITFDAGNATINKYATFMESLRNOKADPKLCYGIPLMDTSTPKYLLVKGANL 60

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DB 121 SRYPTLESKAGVRSOVOLGIIIDLSNIGKIS 153

RESULT 5

Q941G8 PRELIMINARY: PRT: 313 AA.

AC 0941G8: 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE rRNA - glycosidase (EC 3.2.2.22).

GN PAP.

OS Phytolacca aclinosa.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.

OX NCBI\_TaxID=107615;

RN [1]

RP SEQUENCE FROM N.A.

RA Peng X., Yuan J., Qiang B.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.

DR EMBL: AY049785; AAL15442.1; -

DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP. 1.

KW Hydrolase; Toxin.

SQ SEQUENCE 313 AA: 35059 MW: E478CD571C17885 CRC64:

Query Match 75.0%; Score 595; DB 10; Length 313;

Best Local Similarity 71.9%; Pred. No. 1.3e-49;

Matches 110; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLPPTNSPKYLLVLOGANLK 61

DB 23 VNTIIVNGSTISKATFLDNRNKAQPSLKCIGIPLPNTNPKYLVVLOGSNKK 82

QY 62 TTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121

DB 83 TTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCPNPSRVSKININD 142

QY 122 SLPTMEKKAEVNSRNOVOLGIQIILSSDIGIS 154

DB 143 SRYPTLESKAGVRSOVOLGIIIDLSNIGKIS 175

RESULT 6

Q9XFF8 PRELIMINARY: PRT: 315 AA.

AC 09XFF8: 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)

DE rRNA - glycosidase (EC 3.2.2.22).

GN PIP2.

OS Phytolacca insularis.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.

OX NCBI\_TaxID=63744;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20505377; PubMed=11052196;

RA Song S.K., Choi Y., Moon Y.H., Kim S.C., Choi Y.D., Lee J.S.;

RT "Systemic induction of a Phytolacca insularis antiviral protein gene

RT by mechanical wounding, jasmonic acid, and abscisic acid.";

CC -1- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.

DR EMBL: AF141331; AAD32679.1; -

DR HSP: O03464; JAPA.

DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP. 1.

DR PRINTS: PR00396; SHIGARICIN.

DR PROSITE: PS00275; SHIGA\_RICIN; UNKNOWN\_1.

KW Hydrolase; Toxin.

SQ SEQUENCE 315 AA: 35728 MW: F85DE21154B5FA15 CRC64:

Query Match 68.4%; Score 542.5; DB 10; Length 315;

Best Local Similarity 71.1%; Pred. No. 1.6e-44;

Matches 108; Conservative 21; Mismatches 20; Indels 3; Gaps 3;

QY 3 NTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLPPTNSPKYLLVLOGANLK 62

DB 28 NPTTFEAGNATINKYATFMESLRNOAKDPKLCYGIPLPPTNSPKYLLVLOGANLK 87

QY 63 ITLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121

DB 88 ITLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCPNPSRVSKININD 146

QY 122 SLPTMEKKAEVNSRNOVOLGIQIILSSDIGIS 153

DB 147 SSYPALKKRVG-RSRKSOVOLGIQIILSSDIGI 177

RESULT 7

Q8RYA4 PRELIMINARY: PRT: 339 AA.

AC 08RYA4: 01-JUN-2002 (TReMBLrel. 21, Created)

DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Ribosome inactivating protein type I precursor.

OS Phytolacca americana (Common pokeweed) (Virginiian pokeweed).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.

OX NCBI\_TaxID=3527;

RN [1]

RP SEQUENCE FROM N.A.

RA Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.;

RT "Characterization of a novel ethylene-inducible ribosome-inactivating

RT protein exuded from root cultures of Phytolacca americana."

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY071928; AAL61546.1; -

KW Signal.

FT SIGNAL.

SQ SEQUENCE 339 AA: 37978 MW: 7D47BDC2D8DD965F CRC64:

Query Match 66.5%; Score 527; DB 10; Length 339;

Best Local Similarity 66.9%; Pred. No. 5.4e-43;

Matches 103; Conservative 18; Mismatches 29; Indels 4; Gaps 1;

QY 5 ITTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLPPTNSPKYLLVLOGANLK 60

DB 49 ISFDVGSATISKTTTFOESLRNOAKDANKLCIGIPLPNSLMPKYLLELAKLSTSEV 108

QY 61 KTTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 120

DB 109 KTTTLMLRRNNLYVMGYSDPFNGKCRHYHFNIDTSTERTDVENTLCPNPSRVSKININD 168

QY 121 NSLPTMEKKAEVNSRNOVOLGIQIILSSDIGIS 154

DB 169 DSRPTMEKKAEGVSGOVOLGIIILSSDIGIS 202

RESULT 8

P93077 PRELIMINARY: PRT: 302 AA.

AC P93077: 01-MAY-1997 (TReMBLrel. 03, Created)

DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

QY 2 INITTPGAGAAITNKATATMESLRNOKDPKLCXGIPMLPTNSTPKYLLVXLOGANLK 61

Db 25 INITTPDAGAAITNKATATMESLRNOKDPKLCXGIPMLPTNSTPKYLLVXLOGANLK 84

QY 62 TITLMLRRNNLYMGSDPFGNKKCRHYHENDITSTPERDVNTLCSSSSSRVAMSTIYN 122

Db 85 TITLMLRRNNLYMGSDPFGNKKCRHYHENDITSTERTDVNTLCSSSSSRVAMSTIYN 144

QY 122 SLPTMEKKAENVSRNOVQGIQIILSSDICKTS 154

Db 145 SLPTMEKKAENVSRNOVQGIQIILSSDICKTS 177

RESULT	2			
08S946				
ID	08S946	PRELIMINARY:	PRF:	262 AA.
AC	08S946;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	PAP-S2 (Fragment).			
CN	PAP-S2.			
OS	Phytolacca americana (Common pokeweed) (Virginia pokeweed).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta			
OC	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;			
OC	Caryophyllales; Caryophyllaceae; Phytolacca.			
OX	NCBI_TaxID=3527;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Honjo E., Watanabe K.;			
RT	"Cloning of genomic DNA encoding two types of pokeweed antiviral			
RT	protein in seeds, PAP-S1 and PAP-S2, and functional comparison of			
RT	their recombinant proteins with other PAP isoforms.";			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB071855; BAB6350.1; -.			
FT	NON_TER			
FT	1			
FT	262			
FT	NON_TER			
FT	1			
FT	262			
SO	SEQUENCE			
SO	262 AA; 29486 MW; AFD2010A73C9D18B CRC64;			

Query Match	97.5%	Score 773	DB 10	Length 265
Best Local Similarity	97.4%	Pred. No. 6e-67		
Matches 149	Conservative 3	Mismatches 1	Indels 0	Caps 0
QY	2	INTFTFDAGNATINKYATAFMESLRNQAQKDPRLKCYGIPMLPDNTNSTPKYLYLVQGANLK	61	
Db	1	INTFTFDAGNSTINKYATAFMESLRNQAQKDPRLKCYGIPMLPDNTNSTPKYLYLVQGANLK	60	
QY	62	TTTTLRLRRNNLYWACISDPFNGNKCRRHIFNDITSTERDVENTLCCSSSSRYAMISYNN	121	
Db	61	TTTTLRLRRNNLYWACISDPFNGNKCRRHIFNDITSTERDVENTLCCSSSSRYAMISYNN	120	
QY	122	SLYPTMEKKAEYNSRNOVQGLIOLSSDICKIS	154	
Db	121	SLYPTLEKKAERYNSRNOVQGLIOLSSDICKIS	153	

RESULT 3		
08S947		
ID	08S947	PRELIMINARY;
AC	08S947;	PRT; 261 AA.
DT	01-JUN-2002 (TREMBLrel, 21, Created)	
DT	01-JUN-2002 (TREMBLrel, 21, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel, 21, Last annotation update)	
DE	PAP-S1 (Fragment).	
OS	PAISI.	
OS	Physalacca americana (Common pokeberry) (Virginian pokeweed).	
OC	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta;	
OC	Spermatophytidae: Magnoliophyta: eudicotyledons: core eudicots:	
OC	Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.	
OX	NCBI_TaxID=3527;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

RA	Honjo E. Matanabe K.;			
RT	"Cloning of genomic DNA encoding two types of pokeweed antiviral protein in seeds, PAP-S1 and PAP-S2, and functional comparison of their recombinant proteins with other PAP isoforms.";			
RT	submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: AB071854; BABS6349.1;	:	:	:
DR	EMBL: AB071854; BABS6349.1;	:	:	:
FT	NON_TER	1	1	:
FT	NON_TER	261	261	:
SO	SEQUENCE	261 AA;	29199 MW;	DB88B998BEFE1F989 CRC64;
Query Match		84.6%;	Score 670.5;	DB 10; Length 261;
Best Local Similarity		86.3%;	Pred No.5.1e-57;	
Matches 132;	Conservative	8;	Mismatches 12;	Indels 1; Gaps 1

QY 2 INTITDAGNATINKATATMESLRNQADPKKCGIMLPDNTSTPKYLLVYLQGANLK 61

Db 1 INTITDAGNATINKATATMESLRNDKADPKSLCKGIMLPNTNTSYLLVYKLOGASLK 60

QY 62 TITLMLRRNNLVYMGSDPENGKCRHYHFENDITSTERTDVENTLCSSSSRVAMASITNYN 121

Db 61 TITLMLRRNNLVYMGSDPYD-NKCRHYHFENDIKETESDVENTLCPSSNBRAPKATNYN 119

QY 122 SLVPTMEKKAENVSRNQVLGIQLSSPDIGKIS 154

Db 120 GLVPTLEKKAQVTSRNQVQLGIQLSSPDIGKIS 152

RESULT 4			
ID	09ATB3	PRELIMINARY:	PRT: 237 AA.
AC	09ATB3;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
DE	rRNA -glycosidase (EC 3.2.2.22) (Fragment).		
DE	MPAP.		
OS	Phytolacca americana (Common pokeweed) (Virginian pokeweed).		
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:		
OC	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:		
OC	Caryophyllales, Caryophyllaceae, Phytolacca.		
OX	NCBI_TaxId=3527;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RT	Chen D., Wang X., Zhou G.;		
RL	"Pokeweed antiviral protein gene, partial cds.";		
RL	Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: ENDOGYRNAISIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADEOSINE ON THE 28S RRNA.		
CC	-2- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.		
DR	EMBL: AF368910; AKK21951.1; ..		
DR	HSSP: P10297; IQCG.		
DR	InterPro: IPR001574; RIP.		
DR	Pfam: PFO0161; RIP; 1.		
DR	PRINTS: PFO0396; SHIGARICIN.		
DR	PROSITE: PS00275; SHIGA_RICIN; 1.		
KW	Hydrolase; Toxin.		
FT	NON_TER	1	
FT	NON_TER	237	
SEQUENCE	237 AA; 26534 MW; FEADCEED03464783 CRC64;		

Query Match	75.4%	Score 598	DB 10	Length 237
Best Local Similarity	71.9%	Pred. No. 4,86-50		
Matches 110	Conservative 23	Mismatches 20	Indels 0	Gaps 0
QY	2	INTITFDAGNATINKATFTFMSLSRNOAKDPFLKCYGIPMLPDRITSPPKYLVLVLOGANLK	61	
		: : :       :                   :     :       :		
Db	1	VMTIIVYNGSTTISXATFLDLNRNAKDPSLKCYGIPMLPNTNTNPKYLVLEQSSNKK	60	
QY	62	TITLMLRRNNLYVMGYSDPFNGNKCRRYHIFNDITSTERTVENTLSSSSSRVAMSYN	121	
Db	61	TITLMLRRNNLYVMGYSDPFNANKCRHYHIFNDISGTERQDEVTTLCPCNANRSKYN	120	
QY	122	SLYPTMEKKAEVYNSRNOVQIQIQLSSDICKIS	154	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 22.2767 Seconds

(without alignments)  
1424.413 Million cells updates/sec

Title: US-09-978-274A-6

Perfect score: 793

Sequence: 1 MINTTFDAGNATINKYATF.....SRNQVQLGILSSDICKIS 154

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

671580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriophage:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	788	99.4	314	10	P93444
2	773	97.5	262	10	O8S946
3	670.5	84.6	261	10	O8S947
4	598	75.4	237	10	O9ATB3
5	595	75.0	313	10	O941G8
6	542.5	68.4	313	10	O9ATB3
7	527	66.5	339	10	O9ATB3
8	399	50.3	302	10	O8RYA4
9	278.5	35.1	289	10	P93077
10	192.5	24.3	272	10	O941G8
11	192	24.2	279	10	O9ATB3
12	188	23.7	279	10	O9ATB3
13	180	22.7	294	10	O9ATB3
14	177	22.3	294	10	O9ATB3
15	177	22.3	294	10	O9ATB3
16	152	19.2	319	10	O8VWY2

17	129.5	16.3	573	10	O8W2E8	O8W2E8 iris hollan
18	128.5	16.2	279	10	O92T25	O92T25 amarantus
19	125	15.8	300	10	O04356	O04356 iris hollan
20	124.5	15.7	251	10	O48859	O48859 amarantus
21	124	15.6	305	10	O8W4U4	O8W4U4 bougainville
22	123	15.5	300	10	O04357	O04357 iris hollan
23	119	15.0	258	10	O9S9E4	O9S9E4 gelonium mu
24	116	14.6	564	10	O9AVR2	O9AVR2 sambucus eb
25	115.5	14.6	592	10	O8W2E7	O8W2E7 iris hollan
26	115	14.5	278	10	O00980	O00980 luffa cylin
27	115	14.5	563	10	O945S2	O945S2 sambucus ni
28	113	14.2	547	10	O9M6E9	O9M6E9 abrus prec
29	112.5	14.2	103	10	O05148	O05148 seponaria o
30	112.5	14.2	566	10	O04072	O04072 sambucus ni
31	112	14.1	298	10	O04358	O04358 iris hollan
32	112	14.1	541	10	O41174	O41174 ricinus com
33	111.5	14.1	247	10	O9LRE3	O9LRE3 trichosan
34	111.5	14.1	289	10	O94KE4	O94KE4 trichosan
35	110.5	13.9	270	10	O41611	O41611 trichosan
36	110.5	13.9	604	10	O9M654	O9M654 polygonat
37	108	13.6	251	10	O96235	O96235 abrus prec
38	108	13.6	251	10	O96236	O96236 abrus prec
39	108	13.6	251	10	O96237	O96237 abrus prec
40	108	13.6	252	10	O38761	O38761 abrus prec
41	106.5	13.4	580	10	O94BW3	O94BW3 cinna
42	105.5	13.3	289	10	O41216	O41216 trichosan
43	105	13.2	563	10	O04367	O04367 sambucus ni
44	104.5	13.2	581	10	O94BW5	O94BW5 cinna
45	103.5	13.1	580	10	O94BW4	O94BW4 cinna

## ALIGNMENTS

RESULT 1  
P93444 PRELIMINARY: PRT: 314 AA.  
ID P93444  
AC P93444  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE RNA - glycosidase precursor (EC 3.2.2.22).  
OS PAP-S.  
GN Phytolacca americana (Common pokeweed) (Virginiaian pokeweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
OX NCBI\_TaxID=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED;  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J.L., Hoeveler A.;  
RT "cDNA cloning of the gene encoding the Antiviral Protein from the  
RT seeds of Phytolacca americana and its expression in E.coli.";  
RL FEBS Lett. 406:97-100(1997).  
CC -1- CATALYTIC ACTIVITY: ENDOTHEROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
EMBL: X98079; CA66702.1; -;  
DR HSSP; Q03464; IAPA.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP. 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN. 1.  
KW Hydrolyase; Signal; Toxin.  
FT SIGNAL  
FT CHAIN 1 24 POTENTIAL.  
SQ SEQUENCE 314 AA; 35323 MW; A89E3CE5789F9E CRC64;  
Query Match 99.4%; Score 788; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 2.6e-68;  
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: July 2, 2003, 11:37:39
Job time : 7.05346 secs
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OY      4 TTTFDAGNATINKVATEMESLRN--QAKDPKLCYCIGIML-PTDNISPKYLIVLQGAN 59
Db      27 TVKFSLGILGNHNSYSKFIITSMRNALPNAD----IYNILLPSPISGSRRYILMOISNYE 82
OY      60 LKITTLMLRNNLYVMYGSDPFNGNCRCRHIFNDINSTERTDEVENTLCS-----SSSR 113
Db      83 GNTITMAVDVTNYYINGYL-VNGTS---YFENE-----TDQA--LASKFPFGTKSILT 129
OY      114 VAMSINVSLLPYMEKKAEVSNFOVLGIQLISSDIGNI 153
Db      130 LPYSGNYOKLOSVARKE-----RDSLPGLGMALDSALISTL 164

RESULT 15
ABRB_ABRPR STANDARD; PRT; 527 AA.
ID ABRB_ABRPR
AC 006077; P81374;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Abirin-b precursor [Contains: Abirin-b A chain (rRNA N-glycosidase)
   (EC 3.2.2.22); Abirin-b B chain].
OS Abus precatorius (Indian licorice) (Crab's eye)
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
   Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
   eurosids I: Fabales: Fabaceae: Papilionoideae: Abreae; Abrus.
NCBI_TaxID=3816;
RX MEDLINE=93132798; Pubmed=8421313;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isoabpins determined by cDNA
   sequencing. Conservation and significance.";
RJ Mol. Biol. 229:263-267(1993).
[2]
RN SEQUENCE OF 260-527.
RP TISSUE=Seed;
RC MEDLINE=93169023; Pubmed=7763422;
RA Kimura M., Sumizawa T., Funatsu G.;
RT "The complete amino acid sequences of the B-chains of abirin-a and
   abirin-b, toxic proteins from the seeds of Abrus precatorius.";
RL Biosci. Biotechnol. Biochem. 57:166-169(1993).
CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITTING PROTEIN
   SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
   SUBUNITs BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC ABIRIN-A IS MORE TOXIC THAN RICIN.
CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
   FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
   PRECEDES ENDOCYTOSIS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
   specific adenosine on the 28S rRNA.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
   CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
   INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 RICIN B-TYPE LECTIN DOMAINS.
CC -----
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   or send an email to license@isb-sib.ch).
CC -----
DR HSRP; P11140.1AAB.
DR InterPro; IPRO01574; RIP.
DR InterPro; IPRO00772; Ricin_B_lectin.
DR Pfam; PF00161; RIP; 1.
DR Pfam; PF00652; Ricin_B_lectin; 6.
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FT NON\_TER 32 32  
 SQ SEQUENCE 32 AA; 3491 MW; 45BAFEBEE2473CE7 CRC64;  
 Query Match 16.5%; Score 131; DB 1; Length 32;  
 Best Local Similarity 75.0%; Pred. No. 6.2e-07;  
 Matches 24; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 INTTFDAGNATINKYATFMESLRNOAKDPKL 33  
 Db 1 VSTTFDVGATSRISKYTFLESLRNOAKDPKL 32

RESULT 12  
 RIPL\_TRIAN STANDARD; PRT; 294 AA.  
 ID RIPL\_TRIAN  
 AC P5626; 0920Y7;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Type I ribosome-inactivating protein trichoangulina precursor (rRNA N-glycosidase) (EC 3.2.2.22) (RIP) (Trichoangulin).  
 GN TCA.  
 OS Trichosanthes angulina (Snake gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid 1; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 ON NCBI\_TaxID=50544;  
 RX [1]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=ev. Angulina; TISSUE=Seed.  
 RX MEDLINE=99132006; PubMed=9931318;  
 RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,  
 RA Lin J.-Y.;  
 RT "Purification, characterization and molecular cloning of trichoangulin,  
 RT a novel type I ribosome-inactivating protein from the seeds of  
 RT Trichosanthes angulina";  
 RL Biochem. J. 338:211-219(1999).  
 RN [2]  
 RP SEQUENCE OF 20-264.  
 RC TISSUE=Seed;  
 RA Chow L.-P., Kano M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;  
 RT "Amino acid sequence of trichoangulina, a ribosomal-inactivating  
 RT protein from Trichosanthes angulina seeds";  
 RL J. Biomed. Sci. 3:178-186(1996).  
 CC -1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN  
 CC RIBOSOMES.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF055086; AAD02686.1; -  
 DR HSSP: P3185; 1BR7;  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PRO0396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; FALSE\_NEG.  
 KM Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;  
 KM Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 264  
 FT PROPEP 265 294  
 FT ACT\_SITE 177 177  
 FT ACT\_SITE 180 180  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.

FT CARBOHYD 70 70  
 FT CARBOHYD 220 220  
 FT CONFLICT 51 51  
 FT CONFLICT 51 51  
 FT CONFLICT 65 65  
 FT CONFLICT 84 84  
 FT CONFLICT 152 152  
 FT CONFLICT 174 174  
 FT CONFLICT 245 245  
 SQ SEQUENCE 294 AA; 32234 MW; DAAFB8CE3290994 CRC64;  
 Query Match 16.5%; Score 130.5; DB 1; Length 294;  
 Best Local Similarity 27.2%; Pred. No. 1.1e-05;  
 Matches 41; Conservative 30; Mismatches 63; Indels 17; Gaps 6;

OY 2 INTTFDAGNATINKYATFMESLRNOAKDPKLKCYGIPMLPDTNSTPKYL-LVKGANL 60  
 Db 18 IDVSDFLSTARKKSYSSFTLRDLALPTQGTVC-GIPLPSTAGSQMFRFNLNNND 76  
 OY 61 KTTTLMRLNNLYVMGY-SDPFGNCKRYHINDTSTERTDVENTLSSSSRYAMSLN 119  
 Db 77 EIVTVAVNVTNYIYAVRADAVS-----YFFED--TPAEAKLIFAGTKVKLPYSGN 127

OY 120 VNSLYPTMEKRAVNSRNOVOLGIOTSSDI 150  
 Db 128 YDKLOSVGKQ-----RDMIEUGIPALSSAI 153

RESULT 13  
 RIPL\_SAPOF STANDARD; PRT; 236 AA.  
 ID RIPL\_SAPOF  
 AC P27560;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein saporin-3 (SAP-3) (SO-3) (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).  
 GN SAP3.  
 OS Saponaria officinalis (Common soapwort).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.  
 ON NCBI\_TaxID=3572;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92049247; PubMed=1719367;  
 RA Fordham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;  
 RT "Characterisation of saporin genes: In vitro expression and ribosome  
 RT inactivation";  
 RL Mol. Gen. Genet. 229:460-466(1991).  
 CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR  
 CC PHARMACOLOGICAL APPLICATIONS.  
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X59256; CAA1949.1; -  
 DR PIR: S17932; S17932.  
 DR HSSP: P10297; 1QCG.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KM Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;  
 KM Multigene family.

CC TYPE 1 RIP SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: X59260; CAA1953.1; ALT-SEQ.  
DR PIR: S17519; S17519.  
DR HSP: Q03464; IAPA.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA-RICIN; 1.  
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
KW Toxin; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 293  
FT ACT\_SITE 200 200 BY SIMILARITY.  
SQ SEQUENCE 293 AA: 32717 MW: AC85AAC8725DAF2 CRC64;  
Query Match 21.3%; Score 169; DB 1; Length 293;  
Best Local Similarity 29.9%; Pred. No. 1.8e-09;  
Matches 47; Conservative 36; Mismatches 60; Indels 14; Gaps 6;  
QY 6 TFDGAGNATINKYATFMESLRNQAOKDKLKCVCY--IPMLPDTNSTPKYLKLGKCANLKT 62  
DB 28 TLNLAMPASQYSSFLDQIRNNVBDTSL-IVGGTDAVIAIGAPSTDKFLRLNQGR-CT 85  
QY 63 ITTLMRLNNLYVMGYSDPFNGNCKR-YHIFNDITSTERTDVENTLSSSSSRVAMSYN 121  
DB 86 VSLGLRRLNLYVAYLAMADANVNRAYFRNQITSELTALPFEVAVANOKO----LEYG 141  
QY 122 SLPTMEKKAQV-----NSRNOVOLGIISSDGKIS 154  
DB 142 EDQATLEKNAKITTGDSQSKELGGINLITMIDGVN 178  
RESULT 10  
RIP4\_SAPOR  
ID RIP4\_SAPOR STANDARD; PRT; 157 AA.  
AC P27561;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein saporin-4 precursor (SAP-4) (SO-3)  
DE (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).  
GN SAP4.  
OS Saponaria officinalis (Common soapwort).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Saponaria.  
OX NCBI\_TaxID=3572;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92049247; PubMed=1719367;  
RA Fordham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;  
RT "Characterisation of saporin genes: In vitro expression and ribosome  
RT inactivation".  
RL Mol. Gen. Genet. 229:460-466(1991).  
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS  
CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR  
CC PHARMACOLOGICAL APPLICATIONS.  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: X59257; CAA1950.1; ALT-SEQ.  
DR PIR: S17934; S17934.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PROSITE: PS00275; SHIGA-RICIN; PARTIAL.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;  
KW Multigene family.  
FT SIGNAL 1 24  
FT CHAIN 25 >157  
FT NON\_TER 157 157  
SQ SEQUENCE 157 AA: 17520 MW: 22DB3FFDE18286C CRC64;  
Query Match 20.9%; Score 165.5; DB 1; Length 157;  
Best Local Similarity 31.2%; Pred. No. 1.8e-09;  
Matches 43; Conservative 31; Mismatches 57; Indels 7; Gaps 4;  
QY 2 INTTFDAGNATINKYATFMESLRNQAOKDKLKCVCYIPM-LPDTNSTPKYLKLGKCANL 60  
DB 25 VTSITLDPVPTAGQYSSFDKIRNNVCKDNLVYGGTDAVIGPPSKGRFINFQSSR- 83  
QY 61 KTTTLMRLNNLYVMGYSDPFNGNCKR-YHIFNDITSTERTDVENTLSSSSSRVAMSYN 119  
DB 84 GTVSLGKRRLNLYVAYLAMADNVRNRAYFRSEITSELT-----ALFPEATANOKALE 139  
QY 120 YNSLYPTMEKKAQVNSRN 137  
DB 140 YTEDYOSIEKNAQITQED 157  
RESULT 11  
RIP2\_PHYDI  
ID RIP2\_PHYDI STANDARD; PRT; 32 AA.  
AC P34967;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Protein synthesis inhibitor PD-52 (Ribosome-inactivating protein  
DE PD-52) (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).  
OS Phytolacca dioica (Pokeweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
OX NCBI\_TaxID=29725;  
RN (1)  
RP SEQUENCE.  
RC TISSUE-Seed.  
RX MEDLINE=94032487; PubMed=8218414;  
RA Parente A., de Luca P., Bolognesi A., Barbieri L., Battelli M.G.,  
RA Abbondanza A., Sande M.J.W., Gigliano G.S., Tazzari P.L., Stipe F.;  
RT "Purification and partial characterization of single-chain ribosome-  
RT inactivating proteins from the seeds of Phytolacca dioica L.".   
RL Biochim. Biophys. Acta 1216:43-49(1993).  
CC -!- FUNCTION: INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS  
CC IMMUNOTOXIN FOR PHARMACOLOGICAL APPLICATIONS.  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
CC specific adenosine on the 28S rRNA.  
CC -!- TISSUE SPECIFICITY: SEEDS.  
CC -!- PTM: GLYCOSYLATED.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.  
DR PIR: S38528; S38528.  
DR HSP: P10297; 10CG.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PROSITE: PS00275; SHIGA-RICIN; PARTIAL.  
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Glycoprotein;  
KW Toxin.

```

CC EMBL: X69134; CAA4888.1;
DR HSSP: P10297; 10CG.
DR Interpro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KM Multigene family.
FT ACT_SITE 176
SEQUENCE 253 AA; 28553 MW; 161319102AB20539 CRC64;

Query Match 23.3%; Score 184.5; DB 1; Length 253;
Best Local Similarity 30.8%; Pred. No. 4,3e-11;
Matches 49; Conservative 37; Mismatches 62; Indels 11; Gaps 5;

QY 2 INTITFDAGNATINVTATFMESLRNQADPKKCYGIPM-LPDTNSTPKYLKLGANL 60
DB 1 VTSITLDLVNPTAGGYSSVFDKIRNNVDPNKKYGTDAVIGPPSKKEFLINQSSR- 59
QY 61 KTTITMLRRNNLYVWGYSDFPFGNKC-R-YHIFNDITSTERTDVENTLCSSSSRYAMSIN 119
DB 60 GTVSLGLKRDNLVYVAIYALMDNTNVRAYFRSEITSAELT---ALPEATTANQKALE 115

QY 120 YNSLYPTMEKAEV---NSRNQVQIGIQLSSDGIKIS 154
DB 116 YTEDYQSIEKKNQITQGDKSRKELGLDILLTSMQAVN 154

RESULT 8
RIP2_SAPOR
ID RIP2_SAPOR STANDARD: PRT: 292 AA.
AC P27559; Q9SAP5; Q41390;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-2 precursor (SAP-2) (SO-2)
DE (rRNA N-glycosidase) (EC 3.2.2.22).
GN SAP2.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92049247; PubMed=1719367;
RA Fordham-Skelton A.P., Taylor P.E., Hartley M.R., Croy R.R.D.;
RT "Characterisation of saporin genes: In vitro expression and ribosome
RT inactivation."
RL Mol. Gen. Genet. 229:460-466(1991).
RN [2]
RP SEQUENCE OF 25-284 FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=93203250; PubMed=8454624;
RA Barthelemy I., Martineau D., Ong M., Matsunami R., Ling N.,
RA Benatti L., Cavallaro U., Soria M., Lappi D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli."
RL J. Biol. Chem. 268:6541-6548(1993).
CC -I- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR
CC PHARMACOLOGICAL APPLICATIONS.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
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CC -----
CC EMBL: X59255; CAA41948.1;
DR HSSP: P10297; 10CG.
DR Interpro: IPR001574; RIP.
DR Pfam: PF00161; RIP. 1.
DR PROSITE: PS00275; SHIGA_RICIN. 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KM Multigene family.
FT ACT_SITE 200 200
FT CHAIN 25 292
FT SIGNAL 1 24
FT VARIANT 72 72 D->E
SEQUENCE 292 AA; 32810 MW; FA143CE1BE88976 CRC64;

Query Match 23.1%; Score 183.5; DB 1; Length 292;
Best Local Similarity 32.5%; Pred. No. 6,4e-11;
Matches 49; Conservative 33; Mismatches 58; Indels 11; Gaps 5;

QY 2 INTITFDAGNATINVTATFMESLRNQADPKKCYGIPM-LPDTNSTPKYLKLGANL 60
DB 25 VTSITLDLVNPTAGGYSSVFDKIRNNVDPNKKYGTDAVIGPPSKKEFLINQSSR- 83
QY 61 KTTITMLRRNNLYVWGYSDFPFGNKC-R-YHIFNDITSTERTDVENTLCSSSSRYAMSIN 119
DB 84 GTVSLGLKRDNLVYVAIYALMDNTNVRAYFRSEITSAELT---ALPEATTANQKALE 139

QY 120 YNSLYPTMEKAEV---NSRNQVQIGIQL 146
DB 140 YTEDYQSIEKKNQITQGDKSRKELGLDILL 170

RESULT 9
RIP0_DIACA
ID RIP0_DIACA STANDARD: PRT: 293 AA.
AC P24476;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein DAP-30 precursor (Ribosome-inactivating protein)
DE (rRNA N-glycosidase) (EC 3.2.2.22) (Dianthin 30).
OS Dianthus caryophyllus (Carnation) (Clove pink).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
OX NCBI_TaxID=3570;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91355219; PubMed=1840496;
RA Legname G., Bellio P., Gromo G., Modena D., Keen J.N., Roberts L.M.,
RA Legname G.;
RT "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome
RT inactivating protein from Dianthus caryophyllus."
RL Biochim. Biophys. Acta 1090:119-122(1991).
RN [2]
RP SEQUENCE OF 24-82.
RC TISSUE=Leaf;
RX MEDLINE=92037998; PubMed=1936243;
RA Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P.,
RA Huang H.I., Chen H.-C.;
RT "A new class of anti-HIV agents: GAP31, DAPs 30 and 32."
RL FEBS Lett. 291:139-144(1991).
CC -I- FUNCTION: SINGLE-CHAIN RIBOSOME-INACTIVATING PROTEIN, POSSESSING
CC HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
CC AND TO INACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INFECTION AND
CC REPLICATION.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC -----

```

DR EMBL: X15655; CAA33685.1; -  
DR EMBL: S57638; AAB25863.1; -  
DR EMBL: X69135; CAA48889.1; -  
DR EMBL: X64917; CAA46110.1; -  
DR EMBL: A00352; CAA00053.1; -  
DR PIR: S05205; S05205.  
DR HSSP: P10297; 10CG.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PRINTS: PR00396; SHIGARICIN.  
DR PROSITE: PS00275; SHIGA-RICIN. 1.  
KW Plant defense. Protein synthesis inhibitor; Hydrolase; Toxin; signal;  
Multigene family.  
KM SIGNAL. 1  
FT CHAIN. 25 24  
FT PROPE. 278 277 RIBOSOME-INACTIVATING PROTEIN SAPORIN-6.  
FT ACT\_SITE. 200 200 POTENTIAL.  
FT CARBOHD. 283 283 BY SIMILARITY.  
FT VARIANT. 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARIANT. 115 115 E -> D.  
FT VARIANT. 123 123 R -> K.  
FT CONFLICT. 212 212 S -> L (IN REF. 2 AND 4).  
FT CONFLICT. 212 212 I -> T (IN REF. 1; AA SEQUENCE).  
SQ SEQUENCE 299 AA: 33607 MW: 48312958BAE79B CRC64:

Query Match 24.1%; Score 191.5; DB 1; Length 299;  
Best Local Similarity 31.4%; Pred. No. 1,1e-11;  
Matches 50; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

OY 2 INTTFDAGNATINKYATFMESLRQAKDPKLCYGIPI-LPDTNSPKYLLVLOGANL 60  
DB 25 VTSITLDLVNPTAGQYSSFDKIRNNVKDPMKKGCTGTDIAVIGPSKKEFLRINFQSR- 83  
OY 61 KTIILMLRRNLVWYGSDPENGKCR-YHIFNDITSTERDVENTLCCSSSSRYVMSIN 119  
DB 84 GTVSLGKRDMLVYVAYLAMDTNVNRAVYFRSEITSAEST-ALFPEATYANOKALE 139  
OY 120 YNSLYPTMEKRAEV-----NSRNOYQIGIQLSSDIGKS 154  
DB 140 YTEDYQSTIEKNAQITQGDGSRKEGLGIDLLTSMKAVN 178

RESULT 6  
RIP5\_SAPORIN STANDARD: PRT: 253 AA.  
AC Q41389:

DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein saporin-5 (EC 3.2.2.22) (SAP-5) (rRNA N-glycosidase).  
GN SAP5.  
OS Saponaria officinalis (Common soapwort).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Saponaria.  
OX NCBI\_TaxID=3572;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RX MEDLINE=93203250; PubMed=8454624;  
RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N., Benatti L., Cavallaro U., Soria M., Lappi D.A.;  
RT "The expression of saporin, a ribosome-inactivating protein from the plant Saponaria officinalis, in Escherichia coli.";  
RL J. Biol. Chem. 268:6541-6548(1993).  
CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X69131; CAA48885.1; -  
DR EMBL: X69132; CAA48886.1; -  
DR HSSP: P10297; 10CG.  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP.  
DR PROSITE: PS00275; SHIGA-RICIN. 1.  
KW Plant defense. Protein synthesis inhibitor; Hydrolase; Toxin;  
Multigene family.  
KM ACT\_SITE. 176  
FT ACT\_SITE. 176 BY SIMILARITY.  
SQ SEQUENCE 253 AA: 28556 MW: 539693E13D0F594D CRC64:

Query Match 23.3%; Score 184.5; DB 1; Length 253;  
Best Local Similarity 30.8%; Pred. No. 4,3e-11;  
Matches 49; Conservative 37; Mismatches 62; Indels 11; Gaps 5;

OY 2 INTTFDAGNATINKYATFMESLRQAKDPKLCYGIPI-LPDTNSPKYLLVLOGANL 60  
DB 1 VTSITLDLVNPTAGQYSSFDKIRNNVKDPMKKGCTGTDIAVIGPSKKEFLRINFQSR- 59  
OY 61 KTIILMLRRNLVWYGSDPENGKCR-YHIFNDITSTERDVENTLCCSSSSRYVMSIN 119  
DB 60 GTVSLGKRDMLVYVAYLAMDTNVNRAVYFRSEITSAEST-ALFPEATYANOKALE 115  
OY 120 YNSLYPTMEKRAEV-----NSRNOYQIGIQLSSDIGKS 154  
DB 116 YTEDYQSTIEKNAQITQGDGSRKEGLGIDLLTSMKAVN 154

RESULT 7  
RIP7\_SAPORIN STANDARD: PRT: 253 AA.  
AC Q41391:

DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-inactivating protein saporin-7 (SAP-7) (rRNA N-glycosidase) (EC 3.2.2.22).  
GN SAP7.  
OS Saponaria officinalis (Common soapwort).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Saponaria.  
OX NCBI\_TaxID=3572;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RX MEDLINE=93203250; PubMed=8454624;  
RA Barthelmy I., Martineau D., Ong M., Matsunami R., Ling N., Benatti L., Cavallaro U., Soria M., Lappi D.A.;  
RT "The expression of saporin, a ribosome-inactivating protein from the plant Saponaria officinalis, in Escherichia coli.";  
RL J. Biol. Chem. 268:6541-6548(1993).  
CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
CC TYPE 1 RIP SUBFAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DT 16-OCT-2001 (Rel. 40, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Antiviral protein 2 precursor (PAP-II) (Ribosome-inactivating protein)  
 DE (tRNA N-glycosidase) (EC 3.2.2.22).  
 GN PAP2 OR PAP11.  
 OS Phytolacca americana (Common pokeweed) (Virginia pokeweed).  
 OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.  
 OC NCBI\_TaxID=3527.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Leaf;  
 RX MEDLINE=94307398; PubMed=8034016;  
 RA Poyet J.-L., Radom J., Hoeveler A.;  
 RT "Isolation and characterization of a cDNA clone encoding the pokeweed  
 RT antiviral protein II from Phytolacca americana and its expression in  
 RT E. coli.";  
 RL FEBS Lett. 347:268-272(1994).  
 RN [2]  
 RP SEQUENCE OF 26-55.  
 RC TISSUE-Leaf;  
 RX MEDLINE=85023392; PubMed=6091760;  
 RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;  
 RT "Characterization of translational inhibitors from Phytolacca  
 RT americana. Amino-terminal sequence determination and antibody-  
 RT inhibitor conjugates.";  
 RL Biochim. Biophys. Acta 790:154-163(1984).  
 CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. INHIBITS PROTEIN  
 CC SYNTHESIS IN BOTH PROKARYOTES AND EUKARYOTES.  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LATE SUMMER LEAVES.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED PROGRESSIVELY WITH THE AGING OF THE  
 CC PLANT.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC  
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 CC  
 CC EMBL: X78628; CA55342.1;  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP. 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGARICIN. 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KM Toxin; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 ?  
 FT PROPEP 2 310  
 FT ACT\_SITE 197 197 BY SIMILARITY.  
 FT DISULFD 57 284 BY SIMILARITY.  
 FT DISULFD 106 123 BY SIMILARITY.  
 SQ SEQUENCE 310 AA; 34694 MW; 4D3BB001D7259D9F CRC64;  
 Query Match 32.9%; Score 261; DB 1; Length 310;  
 Best Local Similarity 41.2%; Pred. No. 1.5e-18;  
 Matches 63; Conservative 20; Mismatches 60; Indels 10; Gaps 5;  
 QY 3 NTTFDAGNATINKYATFMESLRNQAKPKLKYGIPMLPTNSTPKYLLVKGLOGANKT 62  
 DB 25 SNIVDEVNAPETYSNLTSLREAVKDKLTHCHGMIAWATLTETGPKVVLDLKFGS-CT 83  
 QY 63 ITLMIRNNLVYMGSDPPNGKCRKRYHIFNDITSTERTDEVENTLCCSSSSR--VAMSNY 120  
 DB 84 FTLAIRGNLVLEGYSDIYNG-KCRYRIFK-----SESDAGETVCQDKSKRGTONNIPY 138

QY 121 NSLYPTMEKKAENVSRNOVGLQILSSDIGKI 153  
 DB 139 EKSYKGMESKG--GARTKLGKIKTLKSRNGKI 169  
 RESULT 5  
 RIPE\_SAPOF STANDARD; PRT; 299 AA.  
 AC P20656: 041392;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-OCT-1996 (Rel. 34, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Ribosome-inactivating protein saporin-6 precursor (SAP-6) (SO-6)  
 DE (tRNA N-glycosidase) (EC 3.2.2.22).  
 GN SAP6.  
 OS Saponaria officinalis (Common soapwort).  
 OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllales: Caryophyllales: Saponariaceae: Saponaria.  
 OC NCBI\_TaxID=3572.  
 RN [1]  
 RP SEQUENCE OF 1-283 FROM N.A., AND SEQUENCE OF 25-115; 206-213 AND  
 RP 234-277.  
 RC TISSUE-Leaf;  
 RX MEDLINE=89338421; PubMed=2547612;  
 RA Benatti L., Saccardo M.B., Dani M., Nitli G., Sassano M.,  
 RA Lorenzetti R., Lappi D.A., Soria M.;  
 RT "Nucleotide sequence of cDNA coding for saporin-6, a type-1 ribosome-  
 RT inactivating protein from Saponaria officinalis.";  
 RL Eur. J. Biochem. 183:465-470(1989).  
 RN [2]  
 RP SEQUENCE OF 25-277 FROM N.A.  
 RX MEDLINE=93203250; PubMed=8454624;  
 RA Barthelmy J., Martineau D., Ong M., Matsunami R., Ling N.,  
 RA Benatti L., Cavallaro U., Soria M., Lappi D.A.;  
 RT "The expression of saporin, a ribosome-inactivating protein from the  
 RT plant Saponaria officinalis, in Escherichia coli.";  
 RL J. Biol. Chem. 268:6541-6548(1993).  
 RN [3]  
 RP SEQUENCE OF 275-299 FROM N.A.  
 RC TISSUE-Leaf;  
 RX MEDLINE=92038053; PubMed=1936274;  
 RA Benatti L., Nitli G., Solinas M., Valsasina B., Vitale A.,  
 RA Ceriotti A., Soria M.R.;  
 RT "A Saporin-6 cDNA containing a precursor sequence coding for a  
 RT carboxyl-terminal extension.";  
 RL FEBS Lett. 291:285-288(1991).  
 RN [4]  
 RP SEQUENCE OF 25-72 AND 114-154.  
 RX MEDLINE=90220515; PubMed=2325629;  
 RA Fordham-Skelton A.P., Yarwood A., Croy R.R.D.;  
 RT "Synthesis of saporin gene probes from partial protein sequence data:  
 RT use of inosine-oligonucleotides, genomic DNA and the polymerase chain  
 RT reaction.";  
 RL Mol. Gen. Genet. 221:134-138(1990).  
 CC -1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS  
 CC PROTEIN SYNTHESIS IN ANIMAL CELLS. USEFUL AS IMMUNOTOXIN FOR  
 CC PHARMACOLOGICAL APPLICATIONS.  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -1- TISSUE SPECIFICITY: SEEDS AND LEAVES OF THE PLANT.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC  
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 CC

Query Match.	Best Local Similarity	70.6%	Score 559.5	DB 1:	Length 294:
Matches 112: Conservative 16; Mismatches 22; Indels 3; Gaps 3.					
QY 2 INTITFDAGNATINKYATFMESLRNOAKDPKLCYGIIMLPDPTNSTPKYLLVYKLOGAULK 61					
DB 25 INTITFDVGNATINKYATFMESLRNOAKDPKLCYGIIMLPDPTNSTPKYLLVYKLOGAULK 84					
QY 62 TITLMLRNNLLYVMGSDPFENGNCGRYHIFENDIT-STERTDVENTLCSSSRVAMSYNY 120					
DB 85 TITLMLKNNLLYVMGADTYNG-KCRYHIFKDISNTERBNDVMTLCPNPSRVGKNINY 143					
QY 121 NSLYPTMEKKAEVSRNOVOIGIQLSSDICKI 153					
DB 144 DSSTPALEKKVG-RPRSOVOIGIQLNSGICKI 175					
RESULT 4					
RIP2_PHYAM					
1D RIP2_PHYAM					
Q040772:					
16-Oct-2001 (Rel. 40, Created)					

RESULT 2  
 RIPL\_PHYAM STANDARD; PRT; 313 AA.  
 AC P10297;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Antiviral protein I precursor (PAP-I) (PAP-C) (Ribosome-inactivating  
 protein) (tRNA N-glycosidase) (EC 3.2.2.22).  
 GN PAP1.  
 OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Phytolacaceae; Phytolacca.  
 OC NCBI\_TaxID=3527;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-62.  
 RC TISSUE-Leaf;  
 RX MEDLINE=92003676; PubMed=1912488;  
 RA Lin O., Chen Z.C., Antoniw J.F., White R.F.;  
 RT "Isolation and characterization of a cDNA clone encoding the  
 RL anti-viral protein from Phytolacca americana.";  
 RN Plant Mol. Biol. 17:609-614(1991).  
 RP [2]  
 RP SEQUENCE OF 23-65.  
 RX MEDLINE=89193489; PubMed=2930487;  
 RA Barbieri L., Bolognesi A., Centini P., Falasca A.I., Minghetti A.,  
 RA Garofano L., Guicciardi A., Lippi D., Miller S.P.;  
 RT "Ribosome-inactivating proteins from plant cells in culture.";  
 RL Biochem. J. 257:801-807(1989).  
 RN [3]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Leaf;  
 RX MEDLINE=83290867; PubMed=6885760;  
 RA Houston L.L., Ramakrishnan S., Hermodson M.A.;  
 RT "Seasonal variations in different forms of pokeweed antiviral protein,  
 RL a potent inactivator of ribosomes.";  
 RN J. Biol. Chem. 258:9601-9604(1983).  
 RN [4]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Leaf;  
 RX MEDLINE=85023392; PubMed=6091760;  
 RA Bjorn M.J., Larrick J., Platak M., Wilson K.J.;  
 RT "Characterization of translational inhibitors from Phytolacca  
 RT americana, amino-terminal sequence determination and antibody-  
 RL inhibitor conjugates.";  
 RN Biochim. Biophys. Acta 790:154-163(1984).  
 RN [5]  
 RP SEQUENCE OF 23-54.  
 RC TISSUE-Root;  
 RX MEDLINE=91064383; PubMed=2248976;  
 RA Bolognesi A., Barbieri L., Abbondanza A., Falasca A.I., Carnicelli D.,  
 RA Bateilli M.G., Stirpe F.;  
 RT "Purification and properties of new ribosome-inactivating proteins  
 RT with RNA N-glycosidase activity.";  
 RL Biochim. Biophys. Acta 1087:293-302(1990).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=94016586; PubMed=8411176;  
 RA Monzinge A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D.;  
 RT "The 2.5 A structure of pokeweed antiviral protein.";  
 RL J. Mol. Biol. 233:705-715(1993).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-284.  
 RX MEDLINE=99421320; PubMed=10493577;  
 RA Kurinov I.V., Myers D.E., Irvin J.D., Uckun F.M.;  
 RT "X-ray crystallographic analysis of the structural basis for the  
 RT interactions of pokeweed antiviral protein with its active site  
 RT inhibitor and ribosomal RNA substrate analogs.";  
 RL Protein Sci. 8:1765-1772(1999).  
 CC -!- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN

CC SYNTHESIS IN VITRO.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- TISSUE SPECIFICITY: SPRING LEAVES AND ROOTS.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X55383; CAA39054.1; -  
 DR PIR: S02792; S02792.  
 DR PIR: S13469; S13469.  
 DR PDB: 1PAF; 31-JAN-94.  
 DR PDB: 1PAG; 31-JAN-94.  
 DR PDB: 1OCI; 15-SEP-99.  
 DR PDB: 1OCG; 15-SEP-99.  
 DR PDB: 1OCJ; 15-SEP-99.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KM Toxin; Signal; 3D-structure.  
 FT CHAIN 1 22  
 FT SIGNAL 23 25  
 FT PROPEP 286 313  
 FT ACT\_SITE 198 198  
 FT DISULFID 56 281  
 FT DISULFID 107 128  
 FT STRAND 25 29  
 FT HELIX 35 49  
 FT STRAND 55 56  
 FT TURN 57 58  
 FT TURN 59 61  
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 FT STRAND 71 78  
 FT HELIX 81 81  
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 FT TURN 90 93  
 FT STRAND 94 102  
 FT TURN 103 105  
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 FT TURN 131 132  
 FT STRAND 134 136  
 FT STRAND 139 139  
 FT HELIX 145 152  
 FT TURN 153 153  
 FT TURN 157 158  
 FT STRAND 162 162  
 FT HELIX 164 174  
 FT TURN 175 176  
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 FT HELIX 221 239  
 FT STRAND 241 241  
 FT TURN 242 243  
 FT STRAND 244 252  
 FT TURN 254 255  
 FT STRAND 258 263  
 FT HELIX 264 270



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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:02 ; Search time 6.05346 Seconds  
(without alignments)  
1055.158 Million cell updates/sec

Title: US-09-978-274A-6  
Perfect score: 793  
Sequence: 1 MINTTFDAGNATINKYATF.....SRNOVGLGIQILSSDIGKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	667.5	84.2	261 1 RIPS_PHYAM	P23339 Phytolacca
2	596	75.2	313 1 R1P1_PHYAM	P10297 Phytolacca
3	559.5	70.6	294 1 R1P1_PHYAM	Q03464 Phytolacca
4	261	32.9	310 1 R1P2_PHYAM	Q40772 Phytolacca
5	191.5	24.1	259 1 R1P6_SAPOR	P20656 Saponaria o
6	184.5	23.3	253 1 R1P5_SAPOR	Q41389 Saponaria o
7	184.5	23.3	253 1 R1P1_SAPOR	Q41391 Saponaria o
8	183.5	23.1	292 1 R1P2_SAPOR	P27559 Saponaria o
9	169	21.3	293 1 R1P0_DIACA	P24476 Dianthus ca
10	165.5	20.9	157 1 R1P4_SAPOR	P27561 Saponaria o
11	131	16.5	32 1 R1P2_PHYDI	P34567 Phytolacca
12	130.5	16.5	294 1 R1P1_TRIAN	P56526 Trichosanthe
13	124.5	15.7	236 1 R1P3_SAPOR	P27560 Saponaria o
14	123	15.5	286 1 R1P1_CUCFI	Q9474 Cucumis fig
15	122	15.4	527 1 ABRP_ABRPR	P06077 Abrus prec
16	120	15.1	278 1 R1P1_MIRJA	P21326 Mirabilis j
17	118.5	14.9	286 1 R1P1_MOMCH	P16094 Momordica c
18	118	14.9	250 1 R1P1_LUCFY	P22851 Luffa cylin
19	115	14.5	563 1 NIGB_SAMNI	P33183 Sambucus ni
20	111.5	14.1	282 1 R1P2_BRIDI	P98184 Bryonia dio
21	111.5	14.1	289 1 R1P5_TRIKI	P24478 Trichosanthe
22	111.5	14.1	290 1 R1P1_BRIDI	P33185 Bryonia dio
23	111	14.0	576 1 R1C1_RITCO	P02879 Ricinus dio
24	109.5	13.8	289 1 R1P1_TRIKI	P09989 Trichosanthe
25	109.5	13.8	316 1 R1P0_GELMU	P33186 Gelonium mu
26	108	13.6	528 1 ABRP_ABRPR	P11140 Abrus prec
27	100	12.6	562 1 ABRP_ABRPR	P28590 Abrus prec
28	98.5	12.4	564 1 AGCL_RITCO	P06750 Ricinus com
29	96.5	12.2	286 1 R1P2_MOMBA	P29335 Momordica b
30	87	11.0	319 1 SLTA_BP933	P09385 Bacterioph
31	86	10.8	315 1 SLTA_BP919	P08080 Bacterioph
32	85.5	10.8	280 1 R1P1_HORVU	P22244 Hordeum vul
33	85.5	10.8	280 1 R1P2_HORVU	P04399 Hordeum vul

34	85	10.7	254 1	MLA_VISAL	P81446 viscum albu
35	84.5	10.7	3343 1	YOST_CAEEL	P34616 caenohabdi
36	83	10.5	277 1	R1P1_LUCFY	Q00465 Luffa cylin
37	83	10.5	315 1	SLTA_BP930	P10145 Bacterioph
38	81.5	10.3	1528 1	TP2A_MOUSE	Q01320 mus musculu
39	81	10.2	2875 1	R1P1_TSWS1	P28976 tomato spot
40	79.5	10.0	235 1	PYRF_BARRA	Q44843 bartonella
41	79	10.0	300 1	R1P3_MAIZE	P25891 zea mays (m
42	79	10.0	1076 1	RPOB_ASTIO	P27059 astasia jon
43	77.5	9.8	522 1	GD51_YEAST	P41913 saccharomyc
44	75	9.5	301 1	R1P3_MAIZE	P28522 zea mays (m
45	75	9.5	303 1	ALB3_MAIZE	P10593 zea mays (m

ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD:	PRT:	261 AA.
RIPS_PHYAM	AC	P23339;			
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Antiviral protein S (PAP-S) (Ribosome-inactivating protein) (rRNA				
OS	N-glycosidase) (EC 3.2.2.22).				
OC	Phytolacca americana (Common pokeweed) (Virginian pokeweed).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.				
OX	NCBI:TaxID=3527;				
RN	[1]				
RP	SEQUENCE:				
RC	TISSUE=Seed;				
RX	MEDLINE=91242096; PubMed=1368643;				
RA	Kung S.S., Kimura M., Funatsu G.;				
RT	"The complete amino acid sequence of antiviral protein from the seeds				
RT	of pokeweed (Phytolacca americana).";				
RL	Agric. Biol. Chem. 34:3301-3318(1990).				
CC	-1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN				
CC	SYNTHESIS IN VITRO.				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one				
CC	specific adenosine on the 28S rRNA.				
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.				
CC	TYPE 1 RIP SUBFAMILY.				
DR	PIR; J0401; J0401.				
DR	HSSP; Q03464; IAPA.				
DR	InterPro; IPR001574; RIP.				
DR	Pfam; PF00161; RIP: 1.				
DR	PRINTS; PR00396; SHIGARICIN.				
DR	PROSITE; PS00275; SHIGA_RICIN; 1.				
KW	Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolyase;				
KW	Toxin.				
FT	ACT_SITE 175 175 BY SIMILARITY.				
FT	DISULFID 34 258				
FT	DISULFID 84 105				
FT	DISULFID 261 AA; 29200 MW; D88B99962EB839D CRC64;				
FT	SEQUENCE				
QY	Query Match	84.2%;	Score 667.5;	DB 1;	Length 261;
QY	Best Local Similarity	85.6%;	Pred. No. 7e-59;		
QY	Matches 111;	Conservative 9;	Mismatches 12;	Indels 1;	Gaps 1;
QY	2 INTTFDAGNATINKYATMESLRNOAKOPKLCYGIPLMLPTNSTPKLLVKKLUGANLK 61				
QY	1 INTTFDAGNATINKYATMESLRNAKPKSLKCYGIPLMLPTNSTPKLLVKKLUGASLK 60				
QY	62 TTLMRRNNLVYMGSDPENGKCRVHFNIDTSPERDVNTLCSSSSVYAMSINN 121				
QY	61 TTLMRRNNLVYMGSDPYD-NKCRVHFNIDTSGREYSDVENTLCPSSNPVAKPINTN 119				
QY	122 SLVPTMEKRAEVSRRNOVGLGIQILSSDIGKIS 154				
QY	121 SLVPTMEKRAEVSRRNOVGLGIQILSSDIGKIS 154				
QY	120 GLVPTLEKRAGVTSRRNOVGLGIQILSSDIGKIS 152				



Mol. Gen. Genet. 229, 460-466, 1991  
A:Title: Characterisation of saponin genes: in vitro expression and ribosome inactivation  
A:Reference number: S17932; MUID:92049247; PMID:11719367  
A:Accession: S17933  
A:Molecule type: DNA  
A:Residues: 1-292 <CP9>  
A:Cross-references: EMBL:X59255; GB:563902; NID:g2094853; PIDN:CAA1948.1; PID:g21321  
R:Sorta, M.R.  
Submitted to the EMBL Data Library, October 1992  
A:Reference number: S28539  
A:Accession: S28540  
A:Molecule type: DNA  
A:Residues: 25-283 <SOR>  
A:Cross-references: EMBL:X69132; NID:g21330; PIDN:CAA8886.1; PID:g938284  
R:Ferreras, J.M.; Babilieri, L.; Girbes, T.; Batteilli, M.G.; Rojo, M.A.; Arias, F.J.; Rojo, A.  
Bioschim. Biophys. Acta 1216, 31-42, 1993  
A:Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA  
A:Reference number: S38521; MUID:94032486; PMID:8218413  
A:Accession: S38526  
A:Molecule type: protein  
A:Residues: 25-54 <FER>  
C:Genetics:  
A:Gene: SAP2  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: glycosidase; hydrolase; monomer; toxin  
F.1-24/Domain: signal sequence #status predicted <SIG>  
F.25-292/Product: rRNA N-glycosidase Sap2 #status predicted <MAT>  
F.30-273/Domain: rRNA N-glycosidase homology <RNO>

	Query Match	23.1%	Score	183.5:	DB 1:	Length	292:		
	Best Local Similarity	32.5%*	Pred.	No. 4.2e-10:					
	Matches	49;	Conservative	33;	Mismatches	56;	Indels	11; Gaps	5
Oy	2	INTITFDAGNATINKYATFMESLNRQADPKLCYGIM-LPDTNSTPYKLVKQGANTL	60						
	:	::::: :	:	:	:	:	:	:	:
Dd	25	VTSITLDLVNTAQQSYSSFVDKIRNNVADPNLKVGCTDIAVIGPSKDGLFLINROSSR-	83						
Oy	61	KTITLMERNLLYWGYSDDPENGNKR-YHIFNDITSTERTDEVTALCSSSRASMSRN	119						
	:	: ::  : ::  :: ::	:	:	:	:	:	:	:
Dd	84	GTVSGLGRDNLYVAAYLAMDTNNRAYERSKITSAELT---ALPEEATTANAKALE	139						
Oy	120	YNLSLPTEMKKAEEV----NSRMVOLGIOIL	146						
	:	: ::  : ::  :: ::	:	:	:	:	:	:	:
Dd	140	YTEDIQSLEKNQAIIQTGGDKSKRETLGLIDDL	170						

## RESULT 14

S:17519  
 tRNA N-glycosylase (EC 3.2.2.22) dianthin 30 precursor - clove pink  
 N:Alternate names: DAP30 protein; ribosome-inactivating protein dianthin 30  
 C:Species: *Dianthus carophyllus* (clove pink)  
 C:Date: 20-Feb-1995 #sequence-revision 20-Feb-1995 #text-change 13-Sep-1998  
 C:Accession: S17519; S17685  
 R:Legname, G.; Bellosta, P.; Gromo, G.; Modena, D.; Keen, J.N.; Roberts, L.M.; Lord, J.M.  
 Biochim. Biophys. Acta 1090, 119-122, 1991  
 A:Title: Nucleotide sequence of cDNA coding for dianthin 30, a ribosome inactivating pro  
 A:Reference number: S17519; MUID:91355219; PMID:1840456  
 A:Accession: S17519  
 A:Molecule type: mRNA  
 A:Residues: 1-293 <LEGS>  
 A:Cross-references: EMBL:X59260  
 A:Experimental source: Leaf  
 R:Lee-Huang, S.; Kung, H.; Huang, P.L.; Huang, P.L.; Li, B.O.; Huang, P.; Huang, H.T.; C  
 FEBS Lett. 291, 139-144, 1991  
 A:Title: A new class of anti-HIV agents: GAP31, DAPS 30 and 32.  
 A:Reference number: S17574; MUID:92037998; PMID:1936243  
 A:Accession: S17685  
 A:Molecule type: Protein  
 A:Residues: 24-40, 'X',42-82 <DAP>  
 C:Genetics:  
 A:Gene: dia 30  
 C:function:  
 A:Description: removes a single adenine residue from a highly conserved loop structure F

A:Note: high antiviral potency, but low toxicity to cells in culture or intact animals  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: antiviral; glycosidase; hydrolase; monomer; toxin  
E:1.23/Domain: signal sequence #status predicted <SIG>  
F:12-29/Product: rRNA N-glycosidase diathin 30 #status experimental <MAT>  
F:29-273/Domain: rRNA N-glycosidase homology <RNC>

	Query Match	21.3%	Score 169;	DB 2;	Length 293;					
	Best Local Similarity	29.9%	Pred No.	1e-08;						
	Matches	47;	Conservative	36;	Mismatches	60;	Indels	14;	Gaps	6
Oy	6	TFDAGNATINXYAFPMESLRNQAKDPKLCYG--IPMLPTNSTPKYLVLVLOGANLKT	62							
Dd	28	TLNLNPASQYSSFLDQIRNNVRPSTL-YGGTVAAVIGASTDKFRLNFOPR-GT	85							
Oy	63	ITLMRRNNLLVMGSDPFNGNKCR-YHFNDIISTEEDVENTICSSSSSVAMSINYN	121							
Dd	86	VSLGRRENLYVAVALAMDNAVNVNAFYFKNIITSALCTALPEPVVANMQO---LEVG	141							
Oy	122	SLEYPMKEAEY----NSRNQVOLGIQLISSDIGRSI	154							
Dd	142	EDYAIEKNAKTTTGDSRKELGLGINLLITIMDGVN	178							

## RESULT 15

N-glycosidase (EC 3.2.2.22) Sap4 precursor - common soapwort (fragment)  
 N:Alternate names: Sapopin 4  
 C:Species: *Saponaria officinalis* (common soapwort)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 10-Oct-1997  
 C:Accession: S17934; S15460  
 R:Fordham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Croy, R.R.D.  
 Mol. Gen. Genet. 229, 460-466, 1991  
 A:Title: Characterisation of saporin genes: in vitro expression and ribosome inactivation  
 A:Reference number: S17932; MUID:92049247; PMID:1719367  
 A:Accession: S17934  
 A:Accession: S17934  
 A:Molecule type: DNA  
 A:Residues: 1-157 <FOR>  
 A:Cross-references: EMBL:X59257  
 A>Note: The authors translated the codon AGA for residue 115 as Lys  
 R:Fordham-Skelton, A.P.; Taylor, P.E.; Hartley, M.R.; Croy, R.R.D.  
 submitted to the EMBL Data Library, May 1991  
 A:Description: Characterisation of saporin genes:in vitro expression and ribosome-in  
 A:Reference number: S15458  
 A:Accession: S15460  
 A:Molecule type: DNA  
 A:Residues: 1-127;147-157 <FOR>  
 A:Cross-references: EMBL:X59257  
 C:Superfamily: rRNA N-glycosidase  
 C:Keywords: glycosidase; hydrolase  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-157/Product: rRNA N-glycosidase Sap4 #status predicted <MAT>  
 F:30-157/Domain: rRNA N-glycosidase homology (fragment) <RNC>

Query Match	20.9%	Score 165.5;	DB 2;	Length 157;
Best Local Similarity	31.2%;	Pred. No. 1e-08;		
Matches	43;	Conservative	31;	Mismatches 57;
				Indels 7;
				Gaps 4;

QY 2 INTITTDAGNATINKATFEMSELBNQADPKLKCYGIPM-LPDTNSPKYLLVKLOGANL 60  
Db 25 VTSTITDILVPTAGQYSSFFVDKIRNNVKDNLKYGGDIAVIGPPSKGKFLRINFQSSR- 83  
QY 61 KITITLMRRNLVVMGYSDPFNCKCR-YHIFNDITERTDVENTLCSSSSSVAMISIN 119  
Db 84 GTVSLGKLRNLVVALAMDNTNVNRAIYFRSLITSBELT----ALFPEITANQKALE 139  
QY 120 YNSLYPTMEKKAEVNSRN 137  
Db 140 YTEDYOSIEKNAQITQED 157

Search completed: July 2, 2003, 11:43:01  
Job time : 12.1384 secs





A:Cross-references: EMBL:X55383; NID:g20421; PIDN:CA93054.1; PID:g20422  
 R:Barbieri, L.; Bolognesi, A.; Canali, P.; Falasca, A.I.; Minghetti, A.; Garofano, L.; G  
 Blochm. J. 257, 801-807, 1989  
 A:Title: Ribosome-inactivating proteins from plant cells in culture.  
 A:Reference number: S02792; MUID:89193489; PMID:2930487  
 A:Accession: S02792  
 A:Molecule type: protein  
 A:Residues: 23-55, 'X', 57-65 <BAR>  
 R:Bolognesi, A.; Barbieri, L.; Abbondanza, A.; Falasca, A.I.; Carnicelli, D.; Battelli,  
 Blochm. Biophys. Acta 1087, 293-302, 1990  
 A:Title: Purification and properties of new ribosome-inactivating proteins with RNA N-g  
 A:Reference number: S13469; MUID:91064383; PMID:2248976  
 A:Accession: S13469  
 A:Molecule type: protein  
 A:Residues: 23-54 <BOU>  
 R:Bjorn, M.J.; Larick, J.; Piatek, M.; Wilson, K.J.  
 Blochm. Biophys. Acta 790, 154-163, 1984  
 A:Title: Characterization of translational inhibitors from Phytolacca americana. Amino-t  
 A:Reference number: S32610; MUID:85023392; PMID:6091760  
 A:Accession: S32611  
 A:Molecule type: protein  
 A:Residues: 23-54 <BOU>  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-313/Product: RNA N-glycosidase PAP #status experimental <MAT>  
 F:28-277/Domain: RNA N-glycosidase homology <RNG>

Query Match 75.2%; Score 596; DB 2; Length 313;  
 Best Local Similarity 71.9%; Pred. No. 8, 6e-50;

Matches 110; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

QY 2 INTTFDGNATINATYATFMSLRNQAOKPKLKCYGIPMLPTNTSPKYLKLOGANLK 61  
 Db 23 VNTITVNGSTTISKATFLNDLRNDAKPSLCKTGIPMLPTNPKYLVLELQSSNK 82  
 QY 62 TTLMLRRNNLYVMGYSDPFNGNCRHYHFNIDITSTERTDVENTLSCSSSSSRVMSINYN 121  
 Db 83 TTLMLRRNNLYVMGYSDPFNGNCRHYHFNIDISGERQDVEITLCPNANSVSKNINFD 142  
 QY 122 SLPTMEKKAEVNSRNQVQLGIQLSSDIGKIS 154  
 Db 143 SRYPTLESKAGVKSRSQVQLGIQLSSDIGKIS 175

## RESULT 3

S28421  
 RNA N-glycosidase (EC 3.2.2.22) PAP-alpha - Virginian pokeweed  
 N:Alternate names: antiviral protein alpha-PAP  
 C:Species: Phytolacca americana (Virginian pokeweed)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Jun-2000  
 C:Accession: S28421  
 R:Katoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koitai, A.  
 Plant Mol. Biol. 20, 879-886, 1992  
 A:Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein  
 A:Reference number: S28421; MUID:93099240; PMID:1281338  
 A:Accession: S28421  
 A:Molecule type: DNA  
 A:Residues: 1-294 <KAT>  
 A:Cross-references: EMBL:D10600; NID:g218010; PIDN:BA01451.1; PID:g218011  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase  
 F:30-278/Domain: RNA N-glycosidase homology <RNG>

Query Match 70.6%; Score 559.5; DB 2; Length 294;  
 Best Local Similarity 73.2%; Pred. No. 2, 6e-46;

Matches 112; Conservative 16; Mismatches 22; Indels 3; Gaps 3;

QY 2 INTTFDGNATINATYATFMSLRNQAOKPKLKCYGIPMLPTNTSPKYLKLOGANLK 61  
 Db 25 INTTFDGNATINATYATFMSLRNQAOKPKLKCYGIPMLPTNPKYLVLELQSSNK 84  
 QY 62 TTLMLRRNNLYVMGYSDPFNGNCRHYHFNIDIT-STERTDVENTLSCSSSSSRVMSINYN 120

Db 85 TTLMLRRNNLYVMGYADTYNG-KCRHYHFNIDISTERTDVENTLCPNPSRVCKNINYN 143  
 QY 121 NSLYPTMEKKAEVNSRNQVQLGIQLSSDIGKIS 153  
 Db 144 DSSYPALKERKVG-RPSQVQLGIQLSSDIGKIS 175

## RESULT 4

T12573  
 RNA N-glycosidase (EC 3.2.2.22) - common ice plant  
 N:Alternate names: ribosome-inactivating protein  
 C:Species: Mesembryanthemum crystallinum (common ice plant)  
 C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 21-Jul-2000  
 C:Accession: T12573  
 R:Ripmann, J.F.; Michalowski, C.B.; Nelson, D.E.; Bohmert, H.J.  
 Plant Mol. Biol. 35, 701-709, 1997  
 A:Title: Induction of a ribosome-inactivating protein upon environmental stress.  
 A:Reference number: 217533; MUID:98087998; PMID:9426592  
 A:Accession: T12573  
 A:Status: preliminary; translated from GB/EMBL/DDDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-289 <RIP>  
 A:Cross-references: EMBL:U80072; NID:g1773331; PIDN:AA96824.1; PID:g1773332  
 C:Genetics:  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase

Query Match 35.1%; Score 278.5; DB 2; Length 289;  
 Best Local Similarity 39.3%; Pred. No. 2, 9e-19;

Matches 59; Conservative 28; Mismatches 62; Indels 1; Gaps 1;

QY 4 TTTFDGNATINATYATFMSLRNQAOKPKLKCYGIPMLPTNTSPKYLKLOGANLK 63  
 Db 23 TLVIDIGATEKTYSDPFNGNCRHYHFNIDITSTERTDVENTLSCSSSSSRVMSINYN 82  
 QY 64 TTLMLRRNNLYVMGYSDPFNGNCRHYHFNIDITSTERTDVENTLSCSSSSSRVMSINYN 123  
 Db 83 TSLSRNDLYVGYSDMKRG-KCRHYHFNIDITSTERTDVENTLSCSSSSSRVMSINYN 141  
 QY 124 YPTMEKKAEVNSRNQVQLGIQLSSDIGKIS 153  
 Db 142 YTEIERKAKVRNRKEIGLVNKLTLIPKV 171

## RESULT 5

S46239  
 ribosome-inactivating proteins - Virginian pokeweed  
 C:Species: Phytolacca americana (Virginian pokeweed)  
 C:Date: 10-Dec-1994 #sequence\_revision 12-May-1995 #text\_change 28-May-1999  
 C:Accession: S46239  
 R:Poyet, J.L.; Radom, J.; Hoeveler, A.  
 FEBS Lett. 347, 268-272, 1994  
 A:Title: Isolation and characterization of a cDNA clone encoding the pokeweed antivir  
 A:Reference number: S46239; MUID:94307398; PMID:8034016  
 A:Accession: S46239  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-310 <POV>  
 A:Cross-references: GB:X78628; NID:g517180; PIDN:CA55342.1; PID:g517181  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 F:29-282/Domain: RNA N-glycosidase homology <RNG>

Query Match 32.9%; Score 261; DB 2; Length 310;  
 Best Local Similarity 41.2%; Pred. No. 1, 5e-17;

Matches 63; Conservative 20; Mismatches 60; Indels 10; Gaps 5;

QY 3 NTTFDGNATINATYATFMSLRNQAOKPKLKCYGIPMLPTNTSPKYLKLOGANLK 62  
 Db 25 SNIVDVEAAPTYSNLTSLREAVKDKKLCGHOMINATTLTEOPKRYLVLDLFGS-GT 83  
 QY 63 ITLMLRRNNLYVMGYSDPFNGNCRHYHFNIDITSTERTDVENTLSCSSSSSRVMSINYN 120

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 11.1384 Seconds

(Without alignments)  
1329.163 Million cell updates/sec

Title: US-09-978-274A-6  
Perfect score: 793  
Sequence: 1 MINTIFDAGNATINKYATF.....SRNQVLGIQLSSDGIKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	667.5	84.2	JE0401	antiviral protein
2	396	75.2	S17757	rRNA N-glycosidase
3	559.5	70.6	S28421	rRNA N-glycosidase
4	278.5	35.1	T12573	rRNA N-glycosidase
5	261	32.9	S46239	ribosome-inactivat
6	192.5	24.3	JC4811	betavulgin - beet
7	191.5	24.1	A58823	rRNA N-glycosidase
8	191.5	24.1	S05205	rRNA N-glycosidase
9	190.5	24.0	S29931	rRNA N-glycosidase
10	184.5	23.3	S28539	rRNA N-glycosidase
11	184.5	23.3	S28542	rRNA N-glycosidase
12	183.5	23.1	S28541	rRNA N-glycosidase
13	183.5	23.1	S28541	rRNA N-glycosidase
14	169	21.3	S17519	rRNA N-glycosidase
15	165.5	20.9	S17934	rRNA N-glycosidase
16	165.5	20.9	S17934	rRNA N-glycosidase
17	165.5	20.9	S17934	rRNA N-glycosidase
18	165.5	20.9	S17934	rRNA N-glycosidase
19	165.5	20.9	S17934	rRNA N-glycosidase
20	165.5	20.9	S17934	rRNA N-glycosidase
21	165.5	20.9	S17934	rRNA N-glycosidase
22	165.5	20.9	S17934	rRNA N-glycosidase
23	165.5	20.9	S17934	rRNA N-glycosidase
24	165.5	20.9	S17934	rRNA N-glycosidase
25	165.5	20.9	S17934	rRNA N-glycosidase
26	165.5	20.9	S17934	rRNA N-glycosidase
27	165.5	20.9	S17934	rRNA N-glycosidase
28	165.5	20.9	S17934	rRNA N-glycosidase
29	165.5	20.9	S17934	rRNA N-glycosidase

30	109.5	13.8	316	2	JT0753	rRNA N-glycosidase
31	108	13.6	528	1	TZLSA	abrin-a precursor
32	106.5	13.4	102	2	S11894	rRNA N-glycosidase
33	105.5	13.3	102	2	S17687	rRNA N-glycosidase
34	103.5	13.1	102	2	S17688	rRNA N-glycosidase
35	102	12.9	251	2	C39761	abrin (clone 7.2)
36	100	12.6	528	2	S32431	abrin-d precursor
37	100	12.6	562	1	S16022	abrin-c precursor
38	98.5	12.4	564	1	RLCSAG	agglutinin precurs
39	97.5	12.3	286	2	JC4235	rRNA N-glycosidase
40	96.5	12.2	286	2	S25560	rRNA N-glycosidase
41	91	11.5	319	2	I54695	shiga-like toxin I
42	88	11.1	319	2	S21940	hypothetical prote
43	87.5	11.0	821	2	C64461	hypothetical prote
44	87	11.0	319	2	E90779	shiga toxin 2 subu
45	87	11.0	319	2	G85640	shiga toxin 2 subu

#### ALIGNMENTS

RESULT 1  
JE0401  
antiviral protein - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 07-May-1999  
C:Accession: JE0401  
R:Kung, S.S.; Kimura, M.; Funatsu, G.  
A:Title: The complete amino acid sequence of antiviral protein from the seeds of pok  
A:Reference number: JE0401; MID:91242036; PMID:1368643  
A:Accession: JE0401  
A:Molecule type: Protein  
A:Residues: 1-261 <KUN>  
A:Experimental source: seed  
C:Comment: This protein prevents the replication of a number of plant viruses, and it  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C:Keywords: disulfide bond; glycoprotein  
F:6-254/Domain: rRNA N-glycosidase homology <RNG>  
F:10,44,255/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:34-258,84-105/Disulfide bonds: #status experimental

Query Match 84.2%; Score 667.5; DB 2; Length 261;  
Best Local Similarity 85.6%; Pred. No. 8.9e-57;  
Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 2 INTITFDAGNATINKYATFMESLRNOAKPKLKGIPMLPTNRPKYLLVLOGANLK 61  
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Db 1 INTITFDAGNATINKYATFMESLRNEAKPKSLKCYIPMLPTNSTITKILVLAQASLK 60  
|||||

QY 62 TITMLRRNNLYVMGYSDPFNGKCRHYHFNDDTSTERTDVENTLCCSSSSRYVAMSINYN 121  
|||||  
Db 61 TITMLRRNNLYVMGYSDPYD-NKCRHYHFNDDIKREYDVENTLCPSSNPVRAKPLTNYN 119  
|||||

QY 122 SLVPTMEKKAEVNSRNOVLGIQLSSDGIKIS 154  
|||||  
Db 120 GLVPLEKRAVTSRNEVLGIQLSSDGIKIS 152  
|||||

RESULT 2  
S17757  
rRNA N-glycosidase (EC 3.2.2.22) PAP precursor - Virginian pokeweed  
N:Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-  
C:Species: Phytolacca americana (Virginian pokeweed)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 20-Aug-1999  
C:Accession: S17757; S02792; S13469; S32611  
R:Lin, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.  
Plant Mol. Biol. 17, 609-614, 1991  
A:Title: Isolation and characterization of a cDNA clone encoding the anti-viral prote  
A:Reference number: S17757; MID:92003676; PMID:1912488  
A:Accession: S17757  
A:Molecule type: DNA  
A:Residues: 1-313 <LIN>

Wed Jul 2 12:19:00 2003

us-09-978-274a-8.ra1

Page 8

Search completed: July 2, 2003, 11:40:30  
Job time : 8.0912 secs

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QY 62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKYYNGTCQTT 110  
Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLNLYNGTCQAT 261

RESULT 14  
US-08-477-484B-9  
Sequence 9, Application US/08477484B  
Patent No. 5756699

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,484B  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-477-484B-9

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPYKTEAFLLVAIQWVSEARPKYIENOVKTNFNRAFYDPDPKVINLEEKWKIS 61  
Db 153 GQGSFTEKIEADFLVAIQWVSEARPKYIENOVKTNFNDFSPNDKVLDEENWKIST 212

QY 62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKYYNGTCQTT 110  
Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLNLYNGTCQAT 261

Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLNLYNGTCQAT 261

RESULT 15  
US-08-646-360-9  
Sequence 9, Application US/08646360  
Patent No. 5837491

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996

CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-646-360-9

Query Match 75.4%; Score 429; DB 2; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPYKTEAFLLVAIQWVSEARPKYIENOVKTNFNRAFYDPDPKVINLEEKWKIS 61  
Db 153 GQGSFTEKIEADFLVAIQWVSEARPKYIENOVKTNFNDFSPNDKVLDEENWKIST 212

QY 62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKYYNGTCQTT 110  
Db 213 AIHNSKNGALPKPLELKNADGTWIVLRVDEIKPDVGLNLYNGTCQAT 261

LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-79

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVKTAEFLVLAIQWSEARFYIENQVKTNFNRAFYDDPKVINLEEKWKIS 61

DB 153 GGGSTFEKIEAKFLVLAIQWSEARFYIENQVKTNRDPSPDKVLDEENWKIST 212

QY 62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGTCOTT 110

DB 213 AIHNSKNALPKPLELKNADGTWIVLRVDEIKPDVGLLVNGTCOAT 261

## RESULT 12

US-08-485-286-79  
Sequence 79, Application US/08485286

Patent No. 5646026 5646119

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

NUMBER OF SEQUENCES: 81

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,286

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/378761

FILING DATE: 26-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: BORUCKI, ANDREA T

REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 337-4846

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-485-286-79

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVKTAEFLVLAIQWSEARFYIENQVKTNFNRAFYDDPKVINLEEKWKIS 61

DB 153 GGGSTFEKIEAKFLVLAIQWSEARFYIENQVKTNRDPSPDKVLDEENWKIST 212

QY 62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGTCOTT 110

DB 213 AIHNSKNALPKPLELKNADGTWIVLRVDEIKPDVGLLVNGTCOAT 261

## RESULT 13

US-08-488-113B-9  
Sequence 9, Application US/08488113B

Patent No. 5744580

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

TITLE OF INVENTION: Studinika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

NUMBER OF SEQUENCES: 169

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 110202US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-113B-9

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVKTAEFLVLAIQWSEARFYIENQVKTNFNRAFYDDPKVINLEEKWKIS 61

DB 153 GGGSTFEKIEADFLVLAIQWSEARFYIENQVKTNRDPSPDKVLDEENWKIST 212

COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988,430  
FILING DATE: 19921209  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5416202and, Greta E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-988-430-9

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Db 153 GGGSTFEKIEADFLVLAQWSEARFYIENOVKTNNRFPDPKYNILEEKKGKISE 61  
62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKTVNGTCOTT 110  
213 AIHNSKNALPKPLELNADGTWIVLRVDEIKPDVGLNVTGTCOAT 261

RESULT 10  
US-08-425-336-9  
Sequence 9, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-9

Query Match 75.4%; Score 429; DB 1; Length 261;  
Best Local Similarity 78.9%; Pred. No. 3e-45;  
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

Db 153 GGGSTFEKIEADFLVLAQWSEARFYIENOVKTNNRFPDPKYNILEEKKGKISE 61  
62 AIHNAKNGALPKPLELVDAKGTWIVLRVDEINRDVALLKTVNGTCOTT 110  
213 AIHNSKNALPKPLELNADGTWIVLRVDEIKPDVGLNVTGTCOAT 261

RESULT 11  
US-08-378-761A-79  
Sequence 79, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:

[illegible]

## RESULT 7

```

US-08-501-253A-2
Sequence 2, Application US/08501253A
Patent No. 6146628
GENERAL INFORMATION:
APPLICANT: Uckun, Fatih
APPLICANT: Tumer, Nilgun
TITLE OF INVENTION: Biopharmaceutic Agents Comprising
TITLE OF INVENTION: Recombinant PAP and PAP Mutants
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 6146628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: US
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,253A
FILING DATE: 11-JUL-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kettleberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 600,3230501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-501-253A-2

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	Query Match	Best Local Similarity	79.3%;	Score 451;	DB 4;	length 313;
	Matches	89;	Conservative	6;	Mismatches	14;
					Indels	0;
					Gaps	0;
Qy	2	GVDSPFKTEAFPLVIAIOMVSEARRRKIYENOVKTNPNRAFYDDPKINLEEKGRKISE	61			
Db	176	GWSMFEKTOAEELVIAIQMVSEARRKIYENOVKTNPNRAFNPNPKLNLOETWGIKIST	235			
Qy	62	AHNAKNAKLPKLELVDAKGTKIYLRVEINFDVALKLVNCTCOTT	110			
Db	236	AHDAKNGVLPKPLELVDAKGAKMIYLRVEIKEDVALLVNCGSCOTT	284			

## RESULT 8

US-07-901-707-9  
Sequence 9, Application US/07901707  
Patent No. 5376546  
GENERAL INFORMATION:  
APPLICANT: Bernhad, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Steve F.  
APPLICANT: Lane, Julie A.

? TITLE OF INVENTION: Materials Comprising and Methods of  
 ?  
 ?  
 ? NUMBER OF SEQUENCES: 57  
 ?  
 ? CORRESPONDENCE ADDRESSES:  
 ? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ? ADDRESSEE: Bicknell  
 ? STREET: Two First National Plaza, 20 South Clark  
 ? STREET: Street  
 ? CITY: Chicago  
 ? STATE: Illinois  
 ? COUNTRY: USA  
 ? ZIP: 60603  
 ?  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: Patent In Release #1.0, Version #1.25  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/07/901,707  
 ? FILING DATE: 19920619  
 ?  
 ? CLASSIFICATION: 435  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 07/787,567  
 ? FILING DATE: 04-NOV-1991  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: NO. 5376546and, Greta E.  
 ? REGISTRATION NUMBER: 35,302  
 ? REFERENCE/DOCKET NUMBER: 27129/30910  
 ? TELECOMMUNICATION INFORMATION:  
 ? TELEPHONE: (312) 346-5750  
 ? TELEFAX: (312) 984-5750  
 ?  
 ? TELEX: 25-3856  
 ?  
 ? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 261 amino acids  
 ? TYPE: AMINO ACID  
 ? TOPOLOGY: linear  
 ?  
 ? MOLECULE TYPE: protein  
 ?  
 ? US-07-901-707-9

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Query Match      75.4% ; Pred. 429 ; DB 1 ; Length 261 ;
Best Local Similarity 78.9% ; Pred. No. 3e+5 ;
Matches 86 ; Conservative 5 ; Mismatches 18 ; Indels 0 ; Gaps 0 ;

QY    2   GVDSFPAKTEAFLLVAIQWSEARFRFIENOVKTNNRAFPDPKVINLEEKWGKISE 61
       | | | | | | | | | | | | | | | | | | | | : | : | | | | |
Db     153 GGGSFTKEIENDFLVIAIQWSEARFRFIENOVKTNNRPFSPDVKLDLEEMWKIST 212

QY    62   AIHNAGNALPKPLVDAKTKMIVLVEINDVDALLKVNVCOTC 110
       | | | | | | | | | | | | | | | | | | | | : | : | | | | |
Db     213 AIHNSKNAGALPKPLELNADSTKMIVLRVDIKRPDVGLTNVNVGTCQAT 261

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## RESULT 9

US-0/-988-430-9  
Sequence 9, Application US/07988430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lei, Shau-Ping  
TITLE OF INVENTION: Materials Comprising and Methods of  
Preparation and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois



TISSUE TYPE: Leaf  
US-08-373-858-2

Query Match 79.8%; Score 454; DB 1; Length 313;  
Best Local Similarity 82.6%; Pred. No. 3e-48;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Db 2 GVDSFPVKTEAFLLVAIQWSEARFYIENQVKTNNRAFYDDPKYINLEEKWKIS 61  
176 GVMSFTEKTEAFLLVAIQWSEARFYIENQVKTNNRAFPNPKVLNLOETWGI 235

62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGSCOTT 110  
236 AIHDAKNGVLPKPLELDVDSAGAKWIVLRVDEIKPDVALLNIVGSGCOTT 284

RESULT 2  
US-08-500-611-2  
Sequence 2, Application US/08500611  
Patent No. 5756322  
GENERAL INFORMATION:  
APPLICANT: Tumer, Nilgun E.  
TITLE OF INVENTION: Pokeweed Antiviral Protein Mutants  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500.611  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-611-2

Query Match 79.8%; Score 454; DB 1; Length 313;  
Best Local Similarity 82.6%; Pred. No. 3e-48;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Db 2 GVDSFPVKTEAFLLVAIQWSEARFYIENQVKTNNRAFYDDPKYINLEEKWKIS 61  
176 GVMSFTEKTEAFLLVAIQWSEARFYIENQVKTNNRAFPNPKVLNLOETWGI 235

62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGSCOTT 110  
236 AIHDAKNGVLPKPLELDVDSAGAKWIVLRVDEIKPDVALLNIVGSGCOTT 284

RESULT 3  
US-08-500-694-2  
Sequence 2, Application US/08500694  
Patent No. 880329  
GENERAL INFORMATION:

APPLICANT: Tumer, Nilgun E.  
TITLE OF INVENTION: DNAs Encoding Pokeweed Antiviral Protein  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik  
STREET: 600 South Avenue West  
CITY: Westfield  
STATE: NJ  
COUNTRY: USA  
ZIP: 07090-1497  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/500.694  
FILING DATE: 11-JUL-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REFERENCE/DOCKET NUMBER: OCIRS 3.0-039  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
TELEX: 139-125  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-500-694-2

Query Match 79.8%; Score 454; DB 2; Length 313;  
Best Local Similarity 82.6%; Pred. No. 3e-48;  
Matches 90; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Db 2 GVDSFPVKTEAFLLVAIQWSEARFYIENQVKTNNRAFYDDPKYINLEEKWKIS 61  
176 GVMSFTEKTEAFLLVAIQWSEARFYIENQVKTNNRAFPNPKVLNLOETWGI 235

62 AIHNAKNGALPKPLELDVAKGTWIVLRVDEINRDVALLKYVNGSCOTT 110  
236 AIHDAKNGVLPKPLELDVDSAGAKWIVLRVDEIKPDVALLNIVGSGCOTT 284

RESULT 4  
US-09-005-273-2  
Sequence 2, Application US/09005273  
Patent No. 6137030  
GENERAL INFORMATION:  
APPLICANT: Tumer, Nilgun E.  
TITLE OF INVENTION: PAP MUTANTS THAT EXHIBIT ANTI-VIRAL  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005.273  
FILING DATE: 09-JAN-1998

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 7.0912 Seconds

(without alignments)  
456.414 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569

Sequence: 1 MGVDSPFYKTEAFLLVAIQ.....DEINRDVALLKVNCTCQT 110

Scoring table:

BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2-6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2-6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2-6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2-6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2-6/ptodata/1/1aa/6CTUS.COMB.pep:\*  
6: /cgn2-6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	79.8	313	1	US-08-373-858-2
2	454	79.8	313	1	US-08-500-611-2
3	454	79.8	313	2	US-08-500-694-2
4	454	79.8	313	4	US-09-005-273-2
5	454	79.8	313	4	US-09-005-273-4
6	454	79.8	313	5	PCT-US96-11546-2
7	451	79.3	313	4	US-08-501-253A-2
8	429	75.4	261	1	US-07-901-707-9
9	429	75.4	261	1	US-07-988-430-9
10	429	75.4	261	1	US-08-425-336-9
11	429	75.4	261	1	US-08-378-761A-79
12	429	75.4	261	1	US-08-485-286-79
13	429	75.4	261	1	US-08-488-113B-9
14	429	75.4	261	1	US-08-477-484B-9
15	429	75.4	261	2	US-08-646-360-9
16	429	75.4	261	4	US-08-839-765-9
17	429	75.4	261	4	US-09-136-389-9
18	429	75.4	261	4	US-09-610-838-9
19	429	75.4	261	5	PCT-US92-09487-9
20	399	70.1	305	1	US-08-138-636-2
21	399	70.1	305	1	US-08-319-622A-2
22	399	70.1	305	1	US-08-471-564-2
23	213.5	37.5	251	1	US-08-425-336-109
24	213.5	37.5	251	1	US-08-488-113B-109
25	213.5	37.5	251	1	US-08-477-484B-109
26	213.5	37.5	251	2	US-08-646-360-109
27	213.5	37.5	251	4	US-08-839-765-109

28	213.5	37.5	251	4	US-09-136-389-109	Sequence 109, App
29	213.5	37.5	251	4	US-09-610-838-109	Sequence 109, App
30	212.5	37.3	251	1	US-07-901-707-2	Sequence 2, Appl1
31	212.5	37.3	251	1	US-08-425-336-2	Sequence 2, Appl1
32	212.5	37.3	251	1	US-08-425-336-99	Sequence 99, Appl1
33	212.5	37.3	251	1	US-08-425-336-101	Sequence 101, App
34	212.5	37.3	251	1	US-08-425-336-103	Sequence 103, App
35	212.5	37.3	251	1	US-08-425-336-106	Sequence 106, App
36	212.5	37.3	251	1	US-08-425-336-107	Sequence 107, App
37	212.5	37.3	251	1	US-08-425-336-108	Sequence 108, App
38	212.5	37.3	251	1	US-08-425-336-110	Sequence 110, App
39	212.5	37.3	251	1	US-08-488-113B-2	Sequence 2, Appl1
40	212.5	37.3	251	1	US-08-488-113B-99	Sequence 99, Appl1
41	212.5	37.3	251	1	US-08-488-113B-100	Sequence 100, App
42	212.5	37.3	251	1	US-08-488-113B-101	Sequence 101, App
43	212.5	37.3	251	1	US-08-488-113B-103	Sequence 103, App
44	212.5	37.3	251	1	US-08-488-113B-109	Sequence 109, App
45	212.5	37.3	251	1	US-08-488-113B-109	Sequence 109, App

#### ALIGNMENTS

RESULT 1  
US-08-373-858-2  
Sequence 2, Application US/08373858  
Patent No. 563315  
GENERAL INFORMATION:  
APPLICANT: Kim, Man-Keun  
APPLICANT: Lee, Kwan-Ho  
APPLICANT: Na, Byeong-Kook  
APPLICANT: Jeong, Han-Seung  
APPLICANT: Choi, Kyu-Whan  
APPLICANT: Moon, Young-Ho  
APPLICANT: Jeon, Hong-Seob  
TITLE OF INVENTION: Expression Vector for Phytolecta  
TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,858  
FILING DATE: 18-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Peter  
REGISTRATION NUMBER: 25,351  
REFERENCE/DOCKET NUMBER: 0136/17986-US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7770  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 313 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Phytolacca americana

```
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 332
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion protein
US-09-792-793A-73
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```
Query Match
Best Local Similarity 29.5%; Score 168; DB 9; Length 332;
Matches 44; Conservative 13; Mismatches 32; Indels 8; Gaps 3;
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OY 8 VKTEAFFLLVAIQWSEARFKYIENOVKTNFRAFPDPKYINLEEKWKISEAIIH-NA 66
DB 239 VKDEARFLLIATQMTAEARFRYIQLNLYIKNPNKFNSENKVIQFEVNMKKISTAIYGA 298
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```
OY 67 KNGALPKPLELVDAKGTWKIVLRVDEINRDVALIKYV 103
DB 299 KNGVFNKDYDFGFK-----VRQVKDL--QWGLLMTL 328
```

## RESULT 13

```
US-09-792-793A-76
Sequence 76, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 76
LENGTH: 332
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin Fusion Protein
US-09-792-793A-76
```

```
Query Match
Best Local Similarity 29.5%; Score 168; DB 9; Length 332;
Matches 44; Conservative 13; Mismatches 32; Indels 8; Gaps 3;
```

```
OY 8 VKTEAFFLLVAIQWSEARFKYIENOVKTNFRAFPDPKYINLEEKWKISEAIIH-NA 66
DB 239 VKDEARFLLIATQMTAEARFRYIQLNLYIKNPNKFNSENKVIQFEVNMKKISTAIYGA 298
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```
OY 67 KNGALPKPLELVDAKGTWKIVLRVDEINRDVALIKYV 103
DB 299 KNGVFNKDYDFGFK-----VRQVKDL--QWGLLMTL 328
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## RESULT 14

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US-09-792-793A-36
Sequence 36, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
```

```
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 250
TYPE: PRT
ORGANISM: Momordica charantia
US-09-792-793A-36
```

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Query Match
Best Local Similarity 25.9%; Score 147.5; DB 9; Length 250;
Matches 38; Conservative 14; Mismatches 42; Indels 3; Gaps 1;
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OY 8 VKTEAFFLLVAIQWSEARFKYIENOVKTNFRAFPDPKYINLEEKWKISEAIIHNAK 67
DB 152 VKQAKFFLLVAIQWSEARFKYISDKIPSEKYEETVDEYGTALENNNAKSTAVYNSK 211
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OY 68 ---NGLPKPLELVDAKGTWKIVLRVDEINRDVALIK 101
DB 212 PSTTATKCOLATSPVTISPIWIKVEIKVLGLK 248
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## RESULT 15

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US-09-792-793A-39
Sequence 39, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kirilowii
US-09-792-793A-39
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Query Match
Best Local Similarity 25.7%; Score 146; DB 9; Length 247;
Matches 32; Conservative 22; Mismatches 41; Indels 4; Gaps 2;
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OY 6 FPVTEAFFLLVAIQWSEARFKYIENOVKTNFRAFPDPKYINLEEKWKISEAIIH- 64
DB 142 YNANSAASALMWLIQSTSEARFKYIEQOIGKRVKDFLPSLAISLSENSALSQIOI 201
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OY 65 -NAKNGALPKPLELVDAKGTWKIVLRVDE--INRDVALI 100
DB 202 ASTNNGOFESPFLVILNMONRVTTINVDAGVTSNIAL 240
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Search completed: July 2, 2003, 12:00:37
Job time : 18.1226 secs
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FILED DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 259:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 259:  
US-09-765-527-259

Query Match  
Best Local Similarity 44.7%; Pred. No. 5.3e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFPVKTAEFLVAIQWSEARFKYIENQVKTNFRAPYDPDKVINLEKWKISFA 62  
DB 167 IDNYKPTIASLLVVIQWSEARFTIENQIRNNFOQIRIPANNNTISLEKWKLSFQ 226  
QY 63 IH-NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALIKYVN 104  
DB 227 IRTSGANGMFESEAVELERANGKYYVTAVDQVKPKIALLKFDV 269

RESULT 6  
US-09-765-527-253  
Sequence 253, Application US/09765527  
Patent No. US2002000638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 253:  
US-09-765-527-253

Query Match  
Best Local Similarity 44.7%; Pred. No. 5.7e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFPVKTAEFLVAIQWSEARFKYIENQVKTNFRAPYDPDKVINLEKWKISFA 62  
DB 167 IDNYKPTIASLLVVIQWSEARFTIENQIRNNFOQIRIPANNNTISLEKWKLSFQ 226  
QY 63 IH-NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALIKYVN 104  
DB 227 IRTSGANGMFESEAVELERANGKYYVTAVDQVKPKIALLKFDV 269

RESULT 7  
US-09-765-527-251  
Sequence 251, Application US/09765527  
Patent No. US2002000638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 251:  
US-09-765-527-251

Query Match  
Best Local Similarity 44.7%; Pred. No. 6.2e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFPVKTAEFLVAIQWSEARFKYIENQVKTNFRAPYDPDKVINLEKWKISFA 62  
DB 167 IDNYKPTIASLLVVIQWSEARFTIENQIRNNFOQIRIPANNNTISLEKWKLSFQ 226  
QY 63 IH-NAKNGALPKPLELDVDAKGTWIVLRVDEINRDVALIKYVN 104  
DB 227 IRTSGANGMFESEAVELERANGKYYVTAVDQVKPKIALLKFDV 269

APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
APPLICANT: Neelam, Anil  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT APPLICATION NUMBER: US/09/978,274A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
PRIOR FILING DATE: 2000-10-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 4  
LENGTH: 263  
TYPE: PRT  
ORGANISM: Phytolacca americana  
US-09-978-274A-4

Query Match 99.1%; Score 564; DB 10; Length 263;  
Best Local Similarity 100.0%; Pred. No. 7.9e-56;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GVDSFVKTEAFLLVAIQVSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 61  
DB 155 GVDSFVKTEAFLLVAIQVSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 214  
OY 62 AHNNAKGALEPKLELVDAKGTWIVLRDEINRDVALLKYVNGTCOTT 110  
DB 215 AHNNAKGALEPKLELVDAKGTWIVLRDEINRDVALLKYVNGTCOTT 263

RESULT 3  
US-09-978-274A-2  
Sequence 2, Application US/09978274A  
Patent No. US20020116737A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, Christopher  
APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
APPLICANT: Neelam, Anil  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT APPLICATION NUMBER: US/09/978,274A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
PRIOR FILING DATE: 2000-10-14  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 2  
LENGTH: 314  
TYPE: PRT  
ORGANISM: Phytolacca americana  
US-09-978-274A-2

Query Match 99.1%; Score 564; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 9.9e-56;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GVDSFVKTEAFLLVAIQVSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 61  
DB 178 GVDSFVKTEAFLLVAIQVSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 237  
OY 62 AHNNAKGALEPKLELVDAKGTWIVLRDEINRDVALLKYVNGTCOTT 110  
DB 238 AHNNAKGALEPKLELVDAKGTWIVLRDEINRDVALLKYVNGTCOTT 286

RESULT 4  
US-09-765-527-247  
Sequence 247, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of

NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 247:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 247:  
US-09-765-527-247

Query Match 37.3%; Score 212.5; DB 10; Length 251;  
Best Local Similarity 44.7%; Pred. No. 4.3e-16;  
Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

OY 3 VDSFVKTEAFLLVAIQVSEARFKYIENOVKTNFNRAFPDPKVINLEEKWKISE 62  
DB 145 IDNYKPTETIASLLVLIQVSEARFTIENQIRNPNNTISLEKWKISLQ 204  
OY 63 IHNNAKGALEPKLELVDAKGTWIVLRDEINRDVALLKYV 104  
DB 205 IRTSGANGHSEAVELELRANGKKYVTAVDQYKRIALLKFPD 247

RESULT 5  
US-09-765-527-259  
Sequence 259, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:40:38 ; Search time 17.1226 Seconds

(Without alignments)  
738.742 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569

Sequence: 1 MGVDSFPVKTEAFLLVAIQ.....DEINRDVALLKYVNGTCOTT 110

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications-AA\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	569	100.0	110	10	US-09-978-274A-8	Sequence 8, Appli
2	564	99.1	263	10	US-09-978-274A-4	Sequence 4, Appli
3	564	99.1	314	10	US-09-978-274A-2	Sequence 2, Appli
4	212.5	37.3	251	10	US-09-765-527-247	Sequence 247, App
5	212.5	37.3	293	10	US-09-765-527-259	Sequence 259, App
6	212.5	37.3	332	10	US-09-765-527-253	Sequence 253, App
7	212.5	37.3	332	10	US-09-765-527-251	Sequence 251, App
8	168	29.5	254	9	US-09-792-793A-85	Sequence 85, Appli
9	168	29.5	275	9	US-09-792-793A-35	Sequence 35, Appli
10	168	29.5	327	9	US-09-792-793A-79	Sequence 79, Appli
11	168	29.5	330	9	US-09-792-793A-82	Sequence 82, Appli
12	168	29.5	332	9	US-09-792-793A-76	Sequence 76, Appli
13	168	29.5	332	9	US-09-792-793A-36	Sequence 36, Appli
14	147.5	25.9	247	9	US-09-792-793A-39	Sequence 39, Appli
15	146	23.2	252	10	US-09-347-064-2	Sequence 2, Appli
16	132	23.2	252	10	US-09-347-064-8	Sequence 8, Appli
17	132	23.2	247	9	US-09-792-793A-34	Sequence 34, Appli
18	129	22.7	1447	10	US-09-797-097-2	Sequence 2, Appli
19	85.5	15.0				

20	79	13.9	1024	9	US-10-211-962-84	Sequence 84, Appli
21	77.5	13.6	1454	10	US-09-854-799-22	Sequence 22, Appli
22	77.5	13.6	1454	10	US-09-854-799-26	Sequence 26, Appli
23	77.5	13.6	1454	10	US-09-854-799-32	Sequence 32, Appli
24	76.5	13.4	1101	10	US-09-972-484-52	Sequence 52, Appli
25	76.5	13.4	1101	10	US-09-972-484-54	Sequence 54, Appli
26	76.5	13.4	1452	10	US-09-972-484-2	Sequence 2, Appli
27	74	13.0	1024	9	US-10-211-962-81	Sequence 81, Appli
28	70.5	12.4	251	10	US-09-972-484-59	Sequence 59, Appli
29	70	12.3	1024	9	US-10-211-962-83	Sequence 83, Appli
30	69.5	12.2	798	10	US-09-861-451A-12	Sequence 12, Appli
31	69	12.1	763	10	US-09-815-242-13643	Sequence 13643, A
32	68	12.0	1024	9	US-10-211-962-88	Sequence 88, Appli
33	66	11.6	250	9	US-09-802-208-3	Sequence 3, Appli
34	66	11.6	730	10	US-09-815-242-10741	Sequence 10741, A
35	65.5	11.5	2789	10	US-09-801-574-57	Sequence 57, Appli
36	64.5	11.3	249	9	US-10-153-668-118	Sequence 118, App
37	64.5	11.3	306	9	US-10-153-668-120	Sequence 120, App
38	64.5	11.3	365	9	US-09-809-391-696	Sequence 696, App
39	64	11.2	638	9	US-10-309-437-4	Sequence 4, Appli
40	64	11.2	1024	9	US-10-211-962-86	Sequence 86, Appli
41	63.5	11.2	380	10	US-09-977-653-8	Sequence 8, Appli
42	63.5	11.2	432	9	US-09-746-660A-102	Sequence 102, App
43	63.5	11.2	432	10	US-09-977-653-6	Sequence 6, Appli
44	63.5	11.2	474	9	US-09-738-626-4336	Sequence 4336, Ap
45	63.5	11.2	475	10	US-09-738-363-8	Sequence 8, Appli

## ALIGNMENTS

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RESULT 1
US-09-978-274A-8
; Sequence 8, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
; FILE REFERENCE: 9341-028
; CURRENT APPLICATION NUMBER: US/09/978, 274A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Phytolacca americana
US-09-978-274A-8

Query Match      100.0%   Score 569;   DB 10;   Length 110;
Best Local Similarity 100.0%;   Pred. No. 6,7e-57;
Matches 110;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1      MGVDSFPVKTEAFLLVAIQMWSEARFKYIENOVKTNPNRAFYDPDVINLEEKWGIS 60
      |||||||
DB      1      MGVDSFPVKTEAFLLVAIQMWSEARFKYIENOVKTNPNRAFYDPDVINLEEKWGIS 60
      |||||||

QY      61      EAIHNAKGALEPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTT 110
      |||||||
DB      61      EAIHNAKGALEPKLELVDAKGTWIVLRVDEINRDVALLKYVNGTCOTT 110
      |||||||

RESULT 2
US-09-978-274A-4
; Sequence 4, Application US/09978274A
; Patent No. US20020116737A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher

```

PT New pokeweed antiviral protein mutants - which exhibit anti-viral  
 PR and anti-fungal activity in plants and have reduced phytotoxicity  
 XX  
 PS

Claim 8; -: 64pp; English.

XX  
 CC Proteins AAW14163-W14256 represent new pokeweed antiviral protein (PAP)  
 CC mutants having reduced phytotoxicity but retaining anti-viral or  
 CC anti-fungal activity in plants. The sequences' numbering corresponds to  
 CC the 262 amino acid mature protein. The proteins AAW14165-W14217  
 CC represent serial deletions from the C-terminus whereas sequences  
 CC AAW14218-55 are serial deletions from the N-terminus. Prior to  
 CC processing, the protein contains a 22 amino acid N-terminal signal  
 CC sequence and a 29 amino acid C-terminal extension. PAP is a Type I  
 CC ribosomal inhibitor protein (RIP) that catalyses the removal of a  
 CC specific adenine residue from a highly conserved stem-loop structure in  
 CC the 28S rRNA of eukaryotic ribosomes and also interferes with elongation  
 CC factor-2 binding thus blocking protein translation. The PAP mutants can  
 CC confer broad spectrum virus and fungus resistance to plants without  
 CC causing plant cell death or sterility. They can also confer increased  
 CC resistance to insects, bacteria and nematodes in plants.  
 CC N.B. This sequence is not given in the specification but is generated  
 CC from the wild type sequence reproduced in the specification.

XX  
 SQ Sequence 189 AA;

Query Match 75.2%; Score 596; DB 18; Length 189;  
 Best local Similarity 71.9%; Pred. No. 8.7e-60;

Matches 110; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

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QY 2 INTTFDAGNATINKYATFMESLRNOAKDPKLCYGIPLPDNTSTPKYLLVKGANLK 61
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 1 VNTLIYVGSTTISKYATFLNDLRNEAKDPSLKCYGIPLPNTNTNPKYLVLEQGSNKK 60
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 62 TITLMRRNNLYVMGSDPFGNKKRYHIFNDITSTERDVENTLCCSSSSRYAMSINYN 121
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 61 TITLMRRNNLYVMGSDPFGNKKRYHIFNDISGTERDQVETTLCPNANSRVSKNINF 120
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 122 SLPTMEKKAEVNRSNOVOGIIILSSDIGKIS 154
   | |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 121 SKPTLESKAGVKSQVOIGIILDSNIGKIS 153
   | |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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Search completed: July 2, 2003, 11:39:41  
 Job time : 28.088 secs



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DR   InterPro: IPR001574; RIP.
DR   Pfam: PF00161; RIP. 1.
DR   PRINTS: PR00396; SHIGARICIN.
DR   PROSITE: PS00275; SHIGA_RICIN. 1.
KW   Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal.
KM   Multigene family.
FT   SIGNAL 1 24
FT   CHAIN 25 292
FT   ACT_SITE 200 200
FT   VARIANT 72 72 D -> E.
SQ   SEQUENCE 292 AA; 32810 MW; FA143CE01EB8976 CRC64;

Query Match 30.2%; Score 170.5; DB 1; Length 292;
Best Local Similarity 41.0%; Pred. No. 1.6e-10;
Matches 47; Conservative 12; Mismatches 37; Indels 17; Gaps 4;

QY 7 VKTEAFLLVAIQMSSEARFKYENQVKNFRAPYPPDKVNLSEKMKISEAH-N 65
DB 184 VKNEARFLLAIQMTAEVARFRITQNLVKNFKRDSQNKVQFEVSRKISTAIYGD 243
QY 66 KNGALPKLELVDAKGTWIVLRVDINRDVALLKVV-----NGTCOTT 109
DB 244 KNGVFNKDYDFGFK-----VRQVKDL--QMGLMYLGKPKSSNEANSTAYAT 289

RESULT 10
RIP1_TRIAN STANDARD; PRT; 294 AA.
AC P56626; Q9Z0Y7;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type I ribosome-inactivating protein trichoangulina precursor (rRNA
DE N-glycosidase) (EC 3.2.2.22) (RIP) (Trichoangulin).
GN TCA.
OS Trichoanthus angulina (Snake gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Trichoanthus.
OX NCBI_TaxID=50544;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=cv. Angina; TISSUE=Seed;
RX MEDLINE=99132006; PubMed=991318;
RA Chow L.-P., Chou M.-H., Ho C.-Y., Chuang C.-C., Pan F.-M., Wu S.-H.,
RA Lin J.-Y.;
RT "Purification, characterization and molecular cloning of trichoangulin,
RT a novel type I ribosome-inactivating protein from the seeds of
RT Trichoanthus angulina.";
RL Biochem. J. 338:211-219(1999).
RN [2]
RP SEQUENCE OF 20-264.
RC TISSUE=Seed;
RA Chow L.-P., Kamo M., Lin J.-Y., Wang S.-H., Ueno Y., Tsugita A.;
RT "Amino acid sequence of trichoangulina, a ribosomal-inactivating
RT protein from Trichoanthus angulina seeds.";
RL J. Biomed. Sci. 3:178-186(1996).
-1- FUNCTION: INHIBITS PROTEIN SYNTHESIS BY DEPURINATING 28S RNA IN
CC RIBOSOMES.
-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-1- TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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EMBL AF055086; AM02686.1; -

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DR   HSP: P33185; IBRY.
DR   InterPro: IPR001574; RIP.
DR   Pfam: PF00161; RIP. 1.
DR   PRINTS: PR00396; SHIGARICIN.
DR   PROSITE: PS00275; SHIGA_RICIN. FALSE_NEG.
KW   Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KM   Glycoprotein; Signal.
FT   SIGNAL 1 19
FT   CHAIN 20 264
FT   PROPER 265 294
FT   ACT_SITE 177 177
FT   ACT_SITE 180 180
FT   CARBOHYD 70 70
FT   CARBOHYD 220 220
FT   CONFLICT 51 51 C -> Y (IN REF. 2).
FT   CONFLICT 65 65 W -> R (IN REF. 2).
FT   CONFLICT 84 84 N -> D (IN REF. 2).
FT   CONFLICT 152 152 A -> S (IN REF. 2).
FT   CONFLICT 174 174 C -> S (IN REF. 2).
FT   CONFLICT 245 245 N -> H (IN REF. 2).
SQ   SEQUENCE 294 AA; 32234 MW; DAAFB87CE3290994 CRC64;

Query Match 30.2%; Score 170.5; DB 1; Length 294;
Best Local Similarity 38.2%; Pred. No. 1.6e-10;
Matches 39; Conservative 20; Mismatches 38; Indels 5; Gaps 2;

QY 5 FPKVTEAFLLVAIQMSSEARFKYENQVKNFRAPYPPDKVNLSEKMKISEAH-N 64
DB 159 YDYOSTAALVLVLIQCTAARARYKTEQDVSSHISNFEPNQAVSLSEKMGALSQIOI 218
QY 65 AK---NGALPKLELVDAKGTWIVLRVDINRDVALLKVV-----INRDVALLK 101
DB 219 AARTGHCQGFENVELYNPGTREFSTNIGAVGKNIKILLY 260

RESULT 11
RIP5_SAPOF STANDARD; PRT; 253 AA.
AC Q41389;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein saporin-5 (EC 3.2.2.22) (SAP-5) (rRNA N-
DE glycosidase).
GN SAP5.
OS Saponaria officinalis (Common soapwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=93203250; PubMed=8454624;
RA Barthelemy I., Cavallaro U., Sorio M., Lapoli D.A.;
RA Benatti L., Cavallaro U., Sorio M., Lapoli D.A.;
RT "The expression of saporin, a ribosome-inactivating protein from the
RT plant Saponaria officinalis, in Escherichia coli.";
RL J. Biol. Chem. 268:6541-6548(1993).
-1- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-1- TYPE 1 RIP SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch)
CC -----
DR EMBL: X15655; CAA33685.1; -
DR EMBL: S57638; AAB25863.1; -
DR EMBL: X69135; CAA48889.1; -
DR EMBL: X64917; CAA46110.1; -
DR EMBL: A00352; CAA00055.1; -
DR PIR: S05205; S05205.
DR HSP: P10297; 10CG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN.
DR Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KW Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 277 RIBOSOME-INACTIVATING PROTEIN SAPORIN-6.
FT PROPEP 278 299 POTENTIAL.
FT ACT_SITE 200 200 BY SIMILARITY.
FT CAROHD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 72 72 E -> D.
FT VARIANT 115 115 S -> K.
FT CONFLICT 123 123 S -> L (IN REF. 2 AND 4).
FT CONFLICT 212 212 I -> T (IN REF. 1; AA SEQUENCE).
SQ SEQUENCE 299 AA: 33607 MW: 48C312958BB4E79B CRC64;

Query Match 29.8%; Score 168; DB 1; Length 299;
Best Local Similarity 45.4%; Pred. NO. 2.9e-10;
Matches 44; Conservative 13; Mismatches 32; Indels 8; Gaps 3;

OY 7 VKTEAFLLVIAOMSEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIH-NA 65
DB 184 VKDEIRFLILAIOMSEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIH-NA 243-
OY 66 KNGALPKLELVDAKGTQWIVLRVDEINRDVALLKYV 102
DB 244 KNGVFNKDYDFGFGK-----VRQVKDL--QMGLMLYL 273

RESULT 14
RIP2_BRYDI STANDARD: PRT: 282 AA.
AC P98184; Q9S830;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein bryodin II precursor (rRNA N-
DE glycosidase) (EC 3.2.2.22) (BD2).
OS Bryonia dioica (Red bryony).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OX NCBI_Taxid=3652;
RN [1]
RP SEQUENCE FROM N.A.
RA Stegall C.B., Gawlak S.L., Marguardt H.,
RT "Bryodin 2 a ribosome-inactivating protein isolated from the plant
RL Bryonia dioica."
RL Patent number US5597569, 28-JAN-1997.
RN [2]
RP SEQUENCE OF 22-42.
RC TISSUE=Root;
RX MEDLINE=95151812; PubMed=7849072;
RA Stegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
RA Marguardt H.;
RT "Characterization of ribosome-inactivating proteins isolated from
```

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RT Bryonia dioica and their utility as carcinoma-reactive
RT immunocytogenetics."
RL Blooom; Chem. 5:423-429(1994).
CC - FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1. INHIBITS
CC PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC - CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X13438; -; NOT_ANNOTATED_CDS.
DR HSP: P09989; 1MRJ.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN.
DR Plant defense: Protein synthesis inhibitor; Hydrolase; Toxin;
KW Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 282 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
FT ACT_SITE 183 183 BY SIMILARITY.
FT CAROHD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 282 AA: 30754 MW: C52BE2F6A873769C CRC64;

Query Match 29.3%; Score 165.5; DB 1; Length 282;
Best Local Similarity 42.2%; Pred. NO. 5e-10;
Matches 38; Conservative 13; Mismatches 36; Indels 3; Gaps 2;

OY 15 LVATOMSEARFKYIENOVKTNFRATYDDPKYINLEEKWKISSEAIHNA-KNGALPK 72
DB 175 LVIIQTVEARFKYIEOVSENGTKRPPDPAFLSLONAWGSLSEQIQAOTRGGEFAR 234
OY 73 PLELVDAKGTQWIVLRVDEINRDVALLKY 101
DB 235 PVELRTVSNTPFVTNVNSPYKGIALLLY 264

RESULT 15
RIP0_DICA STANDARD: PRT: 293 AA.
AC P24476;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antiviral protein DAP-30 precursor (Ribosome-inactivating protein)
DE (rRNA N-glycosidase) (EC 3.2.2.22) (Dianthin 30).
OS Dianthus caryophyllus (Carnation) (Clove pink).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Dianthus.
OX NCBI_Taxid=3570;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9135219; PubMed=1840496;
RA Legname G., Bellosta P., Gromo G., Modena D., Keen J.N., Roberts L.M.,
RA Lord J.M.;
RT "Nucleotide sequence of cDNA coding for dianthin 30, a ribosome
RL inactivating protein from Dianthus caryophyllus."
RL Biochim. Biophys. Acta 1090:119-122(1991).
RN [2]
RP SEQUENCE OF 24-82.
RC TISSUE=Leaf;
RX MEDLINE=92037998; PubMed=1936243;
RA Lee-Huang S., Kung H.-F., Huang P.L., Huang P.L., Li B.-Q., Huang P.,
RA Huang H.-I., Chen H.-C.;
```

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RT      "A new class of anti-HIV agents: GAP31, DAPs 30 and 32."
RL      FEBS Lett. 291:139-144(1991).
CC      -1- FUNCTION: SINGLE-CHAIN RIBOSOME-INACTIVATING PROTEIN, POSSESSING
CC      HIGH ANTIVIRAL POTENCY AND LOW TOXICITY TO NORMAL CELLS IN CULTURE
CC      AND TO INTACT ANIMALS. CAPABLE OF INHIBITING HIV-1 INFECTION AND
CC      REPLICATION.
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC      TYPE 1 RIP SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X59260; CAA41953.1; ALT_SEQ.
DR      PIR: S17519; S17519.
DR      HSSP: Q03464; IAPA.
DR      InterPro: IPR001574; RIP.
DR      Pfam: PF00161; RIP; 1.
DR      PRINTS: PR00396; SHIGARICIN.
DR      PROSITE: PS00275; SHIGA_RICIN; 1.
KW      Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW      Toxin; Signal.
FT      SIGNAL      1      23
FT      CHAIN       24      293
FT      ACT_SITE    200      200
SQ      SEQUENCE    293 AA; 32717 MW; AC85AAC8725DAF2 CRC64;

Query Match      28.9%; Score 163; DB 1; Length 293;
Best Local Similarity 43.3%; Pred.No.9.5e-10;
Matches 42; Conservative 13; Mismatches 34; Indels 8; Gaps 3;

OY      7 VKTEAFFLLVAIQWSEAAFKYIENQVKTENFRAFYPPDKVINLEKMGKISEAH-NA 65
DB      184 VKDEARFLIAIQMTAEARFRIOQLVTKNPFNKDSEKNYIQFOVSMKISTALFGDC 243
OY      66 KNGALPKPLELVDAKGTWIVLRVDEINRDVALKXY 102
DB      244 KNGVENKDYDFGFGK-----VRQAKDL--QMGLLKYL 273

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Search completed: July 2, 2003, 11:37:38  
 Job time : 5.28459 secs





Ribosome-inactivating proteins - Virginian pokeweed  
C:Species: Phytolacca americana (Virginian pokeweed)  
C>Date: 10-Dec-1994 #sequence\_revision 12-May-1995 #text\_change 28-May-1999

R:Poyet, J.L.; Radom, J.; Hoeveler, A.  
A:Accession: S46239

A:Title: Isolation and characterization of a cDNA clone encoding the pokeweed antiviral  
F:29-282/Domain: rRNA N-glycosidase homology <RNG>

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-310 <POY>

A:Cross-references: GB:78628; NID:g517180; PIDN:CAAS5342.1; PID:g517181  
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

Query Match 35.1%; Score 200; DB 2; Length 310;  
Best Local Similarity 43.5%; Pred. No. 2,5e-12;  
Matches 47; Conservative 20; Mismatches 29; Indels 12; Gaps 5;

Dy 9 KTEAFELLVAIQWSEARFKYIENQVKTNPNR--FYDPKYNLEEKKGISEAIHA 66  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
182 KNEAEFLLIQWTEASRFKYIENKVKAFEDDANGYPKPALKISLEKMNDVSQVI--A 239

Oy 67 KNG-----ALPKPLELDAGTKMIVLRVDIEINDV--ALLKVYWGCTO 108  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
240 KVGTSGDSITVLTPDDLKDENNKKPWTATYMDLKNDAILLTHV--TCK 285

RESULT 7  
RLCSAG  
agglutinin precursor - castor bean  
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C:Species: Ricinus communis (castor bean)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
C:Accession: A24261; A24210  
J:Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
J.Biol.Chem. 260, 15682-15686, 1985  
A:Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A:Reference number: A24261; MUID:86059449; PMID:2999130  
A:Accession: A24261  
A:Molecule type: mRNA  
A:Residues: 1-564 <ROB>

A:Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701  
R:Araiki, T.; Yoshioaka, Y.; Funatsu, G.  
Biochim. Biophys. Acta 872, 277-285, 1986  
A:Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
A:Reference number: A24210  
A:Accession: A24210  
A:Molecule type: protein  
A:Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-564  
C:Comment: This protein has strong agglutinating activity and weak cytotoxicity compared  
C:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; see:  
E:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-290/Product: agglutinin chain A #status predicted <ACH>  
F:33-281/Domain: rRNA N-glycosidase homology <RNG>  
F:303-564/Product: agglutinin chain B #status experimental <BCH>  
F:319-561,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats  
F:34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F:200,403/Active site: Gly, Arg #status predicted  
F:282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted  
F:324,337,348/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) #status predicted  
F:337,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 33.7%; Score 192; DB 1; Length 564;  
Best Local Similarity 42.3%; Pred. No. 3.1e-11;  
Matches 41; Conservative %18; Mismatches 36; Indels 2; Gaps 1;

Dy 8 VKTEAFPLLVAIQWSEARFKYIENQVKT--NNRAFYDPKYNLEEKKGISEAIHN 65  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 184 IPIILANSFMCVICMISAAAREQYIEGEMRRIRINRNSAPDPSVITLNSWGNLSTALQE 243

Oy 66 AKNGALPKLELVDAWGKTWIVLRVDEINRDVALKY 102

Db 244 SNOGAFASPIQLORRNSKFNVDVSLIPIILALMV 280

RESULT 8

RUCSD

ricin D precursor - castor bean

C:Contains: rRNA N-glycosidase (EC 3.2.2.22)

C:Species: Ricinus communis (castor bean)

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999

C:Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

C:History: K.C.: Halling, A.C.: Murray, E.E.: Tadin, B.F.: Houston, L.L.: Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A:Reference number: A24041; MUID:86067214; PMID:2999712

A:Accession: A24041

A:Molecule type: DNA

A:Residues: 1-576 <HAL>

A:Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R:Tregear, J.W.: Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A:Title: The lectin gene family of Ricinus communis: Cloning of a functional ricin gene

A:Reference number: S20513; MUID:92163016; PMID:1371405

A:Accession: S20513

A:Molecule type: DNA

A:Residues: 1-576 <TRE>

A:Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA70955.1; PID:g21085

R:Lamb, F.I.: Roberts, L.M.: Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A:Title: Nucleotide sequence of cloned cDNA coding for preproricin.

A:Reference number: A24614; MUID:85179479; PMID:3838723

A:Accession: A24614

A:Molecule type: mRNA

A:Residues: 15-75, 'D', '77-550, 'R', '552-576 <LAM>

A:Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R:Yoshitake, S.: Funatsu, G.: Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A:Title: Isolation and sequences of peptic peptides, and the complete sequence of the

A:Reference number: A03372

A:Accession: A03372

A:Molecule type: Protein

A:Residues: 35-97, 'Q', '99-109, 'S', '111-269, 'D', '272-283, 'L', '285-288, 290-302 <YOS>

A:Note: this paper cites the others in the series providing experimental details for

R:Ataki, T.: Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptop

A:Reference number: A24010

A:Accession: A24010

A:Molecule type: Protein

A:Residues: 315-383, 'PS', '386-576 <APA>

R:Funatsu, G.: Kimura, M.: Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A:Title: Primary structure of Ala chain of ricin D.

A:Reference number: A03374

A:Accession: A03374

A:Molecule type: Protein

A:Residues: 315-335, 'N', '337-342, 'NH', '345-362, 364-383, 'PS', '386-399, 'T', '401, 'D', '403, 'E', '527, 'E', '529-564, 'W', '566, 'H', '567-570, 'LI', '573-574, 'F' <FUN>

A:Note: this paper, one of a series, summarizes the experimental details for the dete

R:Ready, M.P.: Kim, Y.: Roberts, J.D.

Proteins 10, 270-278, 1991

A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanis

A:Reference number: A48237; MUID:91352006; PMID:1861863

R:Rutenber, E.: Roberts, J.D.

Proteins 10, 260-269, 1991

A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.

A:Reference number: A48238; MUID:91352005; PMID:1861862

A:Contents: annotation: X-ray crystallography, 2.5 angstroms

R:Katzin, B.J.: Collins, E.J.: Roberts, J.D.

Proteins 10, 251-259, 1991  
 A:Title: Structure of ricin A-chain at 2.5 angstroms.  
 A:Reference number: A48239; MUID:91352004; PMID:1881881  
 A:Contents: annotation: X-ray crystallography, 2.5 angstroms  
 C:Comment: The functional molecule is a disulfide linked dimer of A and B chains, which into the cell of the A chain inhibits protein synthesis. It inactivates the 60S ribosomal subunit.  
 C:Comment: This protein is cytotoxic and very poisonous to animals.  
 C:Superfamily: ricin; RNA N-glycosidase homology  
 C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
 F:1-35/Domain: signal sequence #status predicted <SIG>  
 F:36-302/Product: ricin D chain A #status experimental <ACH>  
 F:46-293/Domain: RNA N-glycosidase homology <RNG>  
 F:313-576/Product: ricin D chain B #status experimental <BCH>  
 F:331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats  
 F:45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:115,156,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F:212/Active site: Glu #status experimental  
 F:215/Active site: Arg #status predicted  
 F:294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental  
 F:336,349,360/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental  
 F:548,569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match 33.7%; Score 192; DB 1; Length 576;  
 Best Local Similarity 39.8%; Pred. No. 3.2e-11;  
 Matches 41; Conservative 19; Mismatches 39; Indels 4; Gaps 2;

Oy 2 GVDSPVYTEAFLLVAIOWVSEARFKYIENOVKT--NENRATYPPDKVINEKKWCKI 59  
 Db 192 GGTOLPLTARSF--ITCIOMISEARFOYLEGEMKTRIRYRSAPDSVITLLESMWRL 249  
 Oy 60 SEAIHNAKNGALPRLPLEVDAGKGTWIVLRVDEINRDVALKY 102  
 Db 250 STAIQESNCGAFASPIQLQRRNGSKFSVYDVSILPIALMVY 292

## RESULT 9

RNA N-glycosidase (EC 3.2.2.22) Sap3 - common soapwort (fragment)  
 N:Alternate names: saporin 3  
 C:Species: Saponaria officinalis (common soapwort)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 20-Aug-1999  
 C:Accession: S17932; S15458  
 R:Fordham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Crox, R.R.D.  
 M:1. Gen. Genet. 229, 460-466, 1991  
 A:Title: Characterisation of saporin genes: in vitro expression and ribosome inactivating  
 A:Reference number: S17932; MUID:92049247; PMID:1719367  
 A:Accession: S17932  
 A:Molecule type: DNA  
 A:Residues: 1-236 <FOR>  
 A:Cross-references: EMBL:X59256; NID:921322; PIDN:CAA1949.1; PID:921323  
 A:Note: the authors translated the codon CTC for residue 75 as Phe and GCA for residue 1  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase; monomer; toxin  
 F:1-221/Domain: RNA N-glycosidase homology (fragment) <RNG>

Query Match 30.9%; Score 176; DB 2; Length 236;  
 Best Local Similarity 44.0%; Pred. No. 4.4e-10;  
 Matches 44; Conservative 15; Mismatches 33; Indels 8; Gaps 3;

Oy 8 VKTEAFLLVAIOWVSEARFKYIENOVKTNFRATYPPDKVINEKKWCKISATIH-NA 66  
 Db 132 VKNEARFLLAIOMTAEARFRYQNLVTKNFPNKENSEKVIQFQNMKSKISKAIYGD 191  
 Oy 67 KNGALPRLPLEVDAGKGTWIVLRVDEINRDVALKYNGT 106  
 Db 192 KNGVFNKDYDFGFGK-----VRQVKDL--QMGLMLVLTGT 224

RESULT 10  
 A58923  
 RNA N-glycosidase (EC 3.2.2.22) saporin S9 - common soapwort  
 C:Species: Saponaria officinalis (common soapwort)

C:Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 01-Mar-2002  
 C:Accession: A58923  
 R:Mastroriotto, M.; Di Marco, A.; Ferranti, P.; Bolognesi, A.; Stirpe, F.; Parente, A.  
 Submitted to the Protein Sequence Database, December 1998  
 A:Description: Saporin-S9, the most basic ribosome-inactivating protein from Saponaria  
 A:Reference number: A58923  
 A:Accession: A58923  
 A:Molecule type: protein  
 A:Residues: 1-253 <MAS>  
 A:Experimental source: seeds  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 C:Keywords: glycosidase; hydrolase; toxin

Query Match 30.1%; Score 171.5; DB 2; Length 253;  
 Best Local Similarity 56.7%; Pred. No. 1.3e-09;  
 Matches 38; Conservative 6; Mismatches 22; Indels 1; Gaps 1;

Oy 8 VKTEAFLLVAIOWVSEARFKYIENOVKTNFRATYPPDKVINEKKWCKISATIH-NA 66  
 Db 160 VKNEARFLLAIOMTAEARFRYQNLVTKNFPNKENSEKVIQFQNMKSKISKAIHGD 219  
 Oy 67 KNGALPRL 73  
 Db 220 KNGVFNK 226

## RESULT 11

RNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd  
 C:Species: Trichosanthes anguina (snake gourd)  
 C:Date: 15-Aug-1996 #sequence\_revision 24-Oct-1997 #text\_change 05-Dec-1997  
 C:Accession: J04840; J0701; J06677  
 R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.  
 Biomed. Sci. 3, 178-186, 1996  
 A:Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein fr  
 A:Reference number: J04840  
 A:Accession: J04840  
 A:Molecule type: protein  
 A:Residues: 1-132, 134-245 <CHO1>  
 A:Experimental source: seed  
 A:Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Ta  
 R:Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.  
 Submitted to JIPID, August 1995  
 A:Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein  
 A:Reference number: J06677  
 A:Accession: J0701  
 A:Molecule type: protein  
 A:Residues: 1-50, 152-245 <CHO2>  
 C:Superfamily: RNA N-glycosidase; RNA N-glycosidase homology  
 F:4-242/Domain: RNA N-glycosidase; hydrolase; phosphoprotein; seed  
 F:51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:70,158,161/Active site: Tyr, Glu, Arg #status predicted  
 F:155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 30.0%; Score 170.5; DB 2; Length 245;  
 Best Local Similarity 38.2%; Pred. No. 1.6e-09;  
 Matches 39; Conservative 20; Mismatches 38; Indels 5; Gaps 2;

Oy \*6 FPKTEAFLLVAIOWVSEARFKYIENOVKTNFRATYPPDKVINEKKWCKISATIH 65  
 Db 140 YDQSTAAALVLTQSTAEARKYITQEOVSSHSSTNPNQAVLSLEKMGALSKQIQ 199  
 Oy 66 AK--NGALPRLPLEVDAGKGTWIVLRVDE--INRDVALKY 102  
 Db 200 ANRTGHGFENPVELYNPDGTRFSVHTSAGVYKKGKIKLLY 241

RESULT 12  
 R10HG2  
 RNA N-glycosidase (EC 3.2.2.22) Sap2 precursor - common soapwort  
 N:Alternate names: ribosome-inactivating protein; saporin 2; saporin S5  
 C:Species: Saponaria officinalis (common soapwort)



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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 15.912 Seconds  
(without alignments)  
1424.413 Million cell updates/sec

Title: US-09-978-274A-8

Perfect score: 569  
Sequence: 1 MGVSDFPKTEAFLLVAIQ.....DEINRVALKRYNGTCOTT 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_rvivirus:\*  
17: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564	99.1	314	10	P93444
2	559	98.2	262	10	O8S946
3	449	78.9	313	10	O941G8
4	438	77.0	339	10	O8RYA4
5	437	76.8	315	10	O9XFF8
6	429	75.4	261	10	O8S947
7	355	62.4	237	10	O9ATB3
8	302	53.1	302	10	P93077
9	213	37.8	272	10	O93418
10	212.5	37.3	258	10	O9S9E4
11	207.5	36.5	279	10	O9MSK6
12	197.5	34.7	279	10	O9AUES3
13	192	33.7	541	10	O41174
14	188.5	33.1	305	10	O8A4U4
15	170.5	30.0	294	10	O93Y65
16	170.5	30.0	294	10	O93Y64

17	154.5	27.2	294	10	O93Y66	O93Y66 dianthus ch
18	149	26.2	289	10	P93261	P93261 mesembryant
19	147.5	25.9	549	10	O9FV22	O9FV22 cinanomum
20	147.5	25.9	580	10	O94BW3	O94BW3 cinanomum
21	147.5	25.9	581	10	O94BW5	O94BW5 cinanomum
22	146.5	25.7	270	10	O9S4O5	O9S4O5 cinanomum
23	146.5	25.7	319	10	O8VWY2	O8VWY2 spiracila ol
24	146	25.7	289	10	O94KE4	O94KE4 trichosanthe
25	145	25.5	247	10	O9LRE3	O9LRE3 trichosanthe
26	145	25.5	289	10	O41216	O41216 trichosanthe
27	145	25.5	382	10	O8S4A3	O8S4A3 abrus prece
28	144	25.3	270	10	O41611	O41611 trichosanthe
29	143.5	25.2	279	10	O92T25	O92T25 amarantulus
30	143.5	25.2	284	10	O96322	O96322 amarantulus
31	143.5	25.2	580	10	O94BM4	O94BM4 cinanomum
32	138	24.3	293	10	O8VYU0	O8VYU0 jatropa cu
33	137.5	24.2	251	10	O48859	O48859 amarantulus
34	137.5	24.2	278	10	O00980	O00980 luffa cylin
35	137	24.1	286	10	O9FUV7	O9FUV7 momordica c
36	135	23.7	252	10	O38761	O38761 abrus prece
37	134	23.6	565	10	O04071	O04071 sambucus nl
38	134	23.6	566	10	O04072	O04072 sambucus nl
39	133.5	23.5	604	10	O9M654	O9M654 polygonatum
40	133	23.4	293	10	O8S4S2	O8S4S2 jatropa cu
41	133	23.4	547	10	O9M6E9	O9M6E9 abrus prece
42	132.5	23.3	570	10	O22415	O22415 sambucus nl
43	132.5	23.3	603	10	O9M653	O9M653 polygonatum
44	132	23.2	264	10	O9F5H2	O9F5H2 momordica c
45	132	23.2	286	10	O41257	O41257 momordica c

## ALIGNMENTS

## RESULT 1

P93444 ID P93444 PRELIMINARY: PRT: 314 AA.

AC P93444: 01-MAY-1997 (TRENBLREL. 03, Created)

DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)

DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)

DE rRNA-glycosidase precursor (EC 3.2.2.22).

GN PAP-S.

OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:

OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:

OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.

OX NCBI\_TaxID=3527;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SEED:

RC MEDLINE=97263479; PubMed=9109394;

DR HSSP: Q03464; IAPA.

DR InterPro: IPR001574; RIP.

DR Pfam: PF00161; RIP.

DR PRINTS: P000396; SHIGARICIN.

DR PROSITE: PS00275; SHIGA\_RICIN. 1.

KT Hydrolyase; Signal; Toxin.

FT SIGNAL 1 24

FT CHAIN 25 314

SO SEQUENCE 314 AA; 35323 MW; A89E3CE57789F9E CRC64;

Query Match 99.1%; Score 564; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 3e-52;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY 2 GVDSEPVKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 61
DB 178 GVDSEPVKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 237
QY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQT 110
DB 238 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQT 286

RESULT 2
08S946 PRELIMINARY: PRT: 262 AA.
AC 08S946:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE PAP-S2 (Fragment).
GN PAP-S2.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Honjo E., Watanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB01855; BAB86350.1; -.
FT NON-TER 1
FT SEQUENCE 262 AA: 29486 MW: AF2D010A73C9D18B CRC64:

Query Match 98.2%; Score 559; DB 10; Length 262;
Best Local Similarity 99.1%; Pred. No. 8.3e-52;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

QY 2 GVDSEPVKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 61
DB 154 GVDSEPVKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 213
QY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQT 110
DB 214 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQT 262

RESULT 3
0941G8 PRELIMINARY: PRT: 313 AA.
AC 0941G8:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE rRNA-glycosidase (EC 3.2.2.22).
GN PAP.
OS Phytolacca acinosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=107615;
RN [1]
RP SEQUENCE FROM N.A.
RA Peng X., Yuan J., Qiang B.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL; AY049785; AAL15442.1; -.
DR InterPro; IPR001574; RIP.
PFam; PF00161; RIP; 1.

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KW Hydrolase; Toxin.
SQ SEQUENCE 313 AA: 35059 MW: E478ECD571C17885 CRC64:

Query Match 78.9%; Score 449; DB 10; Length 313;
Best Local Similarity 81.7%; Pred. No. 6.3e-40;
Matches 89; Conservative 5; Mismatches 15; Indels 0; Gaps 0:

QY 2 GVDSEPVKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 61
DB 176 GVTSTFTEKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 235
QY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQT 110
DB 236 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQT 284

RESULT 4
08RYA4 PRELIMINARY: PRT: 339 AA.
AC 08RYA4:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Ribosome inactivating protein type 1 precursor.
OS Phytolacca americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.;
RT "Characterization of a novel ethylene-inducible ribosome-inactivating
RT protein exuded from root cultures of Phytolacca americana."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071928; AAL61546.1; -.
FT SIGNAL 1
FT SEQUENCE 339 AA: 37978 MW: 7D47BDC2DED965F CRC64:

Query Match 77.0%; Score 438; DB 10; Length 339;
Best Local Similarity 80.4%; Pred. No. 1.1e-38;
Matches 86; Conservative 4; Mismatches 17; Indels 0; Gaps 0:

QY 2 GVDSEPVKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 61
DB 203 GVSFTEKTEAFLLVAIOMVSEARFKYIENQVKTNFRAFYDDPKVINLEEKWKIS 262
QY 62 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQ 108
DB 263 AIHNAKNGALPKPELVDAKGTWIVLRVDEINRDVALKYVNGTCQ 309

RESULT 5
09XFF8 PRELIMINARY: PRT: 315 AA.
AC 09XFF8:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE rRNA-glycosidase (EC 3.2.2.22).
GN PIP2.
OS Phytolacca insularis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.
OX NCBI_TaxID=63744;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20505377; PubMed=11052196;
RA Song S.K., Choi Y., Moon Y.H., Kim S.G., Choi Y.D., Lee J.S.;
RT "Systemic induction of a Phytolacca insularis antiviral protein gene
RT by mechanical wounding, jasmonic acid, and abscisic acid."

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RL Plant Mol. Biol. 43:439-450(2000).
CC -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF141331; AAD32679.1; -.
DR HSSP: 003464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
KM Hydrolyase; Toxin.
SQ SEQUENCE 315 AA: 35728 MW; F85DE21154B5FA15 CRC64;

Query Match 76.8%; Score 437; DB 10; Length 315;
Best Local Similarity 78.9%; Pred. No. 1.2e-38;
Matches 86; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 2 GVDSPVTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPPKYINLEEKKGKISE 61
DB 179 GVDITNEKTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPAKYINLEETGKIST 238
62 AIHNAKNGALPKPLDVLDAKGTKWIVLRVDEINRDPVALKYNVCQT 110
239 AIHDAKNGALTKPLDLINEDGTKWIVLRVDEIKPVGLLNVCYDGTCT 287

RESULT 6
QY 08S947 PRELIMINARY: PRT: 261 AA.
AC 08S947:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE PAP-SI (Fragment).
GN PAPSI.
OS Physiolacca americana (Common pokeberry) (Virginian pokeweed);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OC NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Honjo E., Watanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-SI and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBD databases.
DR EMBL: AB071854; BAB86349.1; -.
FT NON_TER 1 1
FT NON_TER 261 261
SQ SEQUENCE 261 AA: 29199 MW; D88B998BFEF1F989 CRC64;

Query Match 75.4%; Score 429; DB 10; Length 261;
Best Local Similarity 78.9%; Pred. No. 7e-38;
Matches 86; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 GVDSPVTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPPKYINLEEKKGKISE 61
DB 133 GCGSTKEKTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPDKYIDLEENNGKIST 212
62 AIHNAKNGALPKPLDVLDAKGTKWIVLRVDEINRDPVALKYNVCQT 110
213 AIHNAKNGALPKPLDVLDAKGTKWIVLRVDEIKPVGLLNVCYDGTCT 261

RESULT 7
QY 09ATB3 PRELIMINARY: PRT: 237 AA.
AC 09ATB3:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE tRNA -glycosidase (EC 3.2.2.22) (Fragment).

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GN MPAP.
OS Physiolacca americana (Common pokeberry) (Virginian pokeweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Phytolaccaceae; Phytolacca.
OC NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen D., Wang X., Zhou G.;
RT "Pokeweed antiviral protein gene, partial cds.";
RL Submitted (JAN-2001) to the EMBL/Genbank/DBD databases.
CC -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AF338910; AAK21951.1; -.
DR HSSP: P10297; IOCG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KM Hydrolyase; Toxin.
FT NON_TER 1 1
FT NON_TER 237 237
SQ SEQUENCE 237 AA: 26534 MW; FE4ADCEB03464783 CRC64;

Query Match 62.4%; Score 355; DB 10; Length 237;
Best Local Similarity 83.3%; Pred. No. 5.3e-30;
Matches 70; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 GVDSPVTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPPKYINLEEKKGKISE 61
DB 154 GVMSTKEKTEAFELVAIOMVSEARFYIENOVNTNFRAPYPPKYLINLEETGKIST 213
62 AIHNAKNGALPKPLDVLDAKGTKW 85
214 AIHNAKNGALPKPLDVLDAKGTKW 237

RESULT 8
QY 093077 PRELIMINARY: PRT: 302 AA.
AC 093077:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE tRNA -glycosidase (EC 3.2.2.22).
GN RIP.
OS Clerodendrum aculeatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiaceae; Clerodendrum.
OC NCBI_TaxID=54208;
RN [1]
RP SEQUENCE FROM N.A.
RA Kumar D., Verma H.N., Tuleja N., Tewari K.K.;
RT "Cloning and characterization of a gene encoding an antiviral protein
RT from Clerodendrum aculeatum L.";
RL Plant Mol. Biol. 33:745-751(1997).
CC -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RRNA.
CC -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: X96474; CA65328.1; -.
DR EMBL: X96583; CA65402.1; -.
DR HSSP: P10297; IOCG.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP; 1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA_RICIN; 1.
KM Glycosidase; Hydrolyase; Toxin.
SQ SEQUENCE 302 AA: 33955 MW; B0561C3918C2E6A2 CRC64;

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Query Match 53.1%; Score 302; DB 10; Length 302;  
 Best Local Similarity 58.9%; Pred. No. 3.4e-24;  
 Matches 63; Conservative 11; Mismatches 33; Indels 0; Gaps 0;

QY 2 GVDSFVKTEAFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISEA 61  
 DB 176 GVRATKEAEAFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKIST 235  
 QY 62 AHNKNGALPKPELVDAKGTWIVLRVDEINRDVALIKYNGTCQ 108  
 DB 236 PIRNANGVISPPLNLSNGEDPMWTVTRVDEIKPIYALLNFGSGTCQ 282

## RESULT 9

Q39418 PRELIMINARY: PRT: 272 AA.  
 ID Q39418  
 AC Q39418;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Antiviral protein precursor (Ribosome-inactivating protein) (RNA N-glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)  
 DE (BETAVOLGIN) (BVG).  
 GN RIP OR BETAVOLGIN OR BVG.  
 OS Beta vulgaris (Sugar beet).  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots;  
 OC Caryophyllales: Caryophyllales; Chenopodiaceae; Beta.  
 RX NCBI\_TaxID=3555;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE=SEEDLING;  
 RA MEDLINE=96235141; Pubmed=8666251;  
 RA Hottung E., Majant H., Jeske H., Mundry K.-W.;  
 RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from  
 RT Beta vulgaris vulgaris (mangold).";  
 RL Gene 170:233-236(1996).  
 CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS, AND PROTEIN  
 CC SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR  
 CC SUICIDE UPON INVASION BY A VIRUS.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING  
 CC PROTEINS.  
 CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.  
 CC EMBL: X85967; CA59952.1; .  
 CC DR HSSP: Q03464; IAPA.  
 CC DR InterPro: IPR001574; RIP.  
 CC Pfam: PF00161; RIP; 1.  
 CC DR PRINTS: PR00396; SHIGARICIN.  
 CC DR PROSITE: PS00275; SHIGA\_RICIN; FALSE\_NEG.  
 CC KW Hydrolase; Glycosidase; Antiviral; Protein synthesis inhibitor; Toxin;  
 CC MultiGene family; Signal.  
 CC FT SIGNAL 1 23 BY SIMILARITY.  
 CC FT CHAIN 24 272 ANTIVIRAL PROTEIN.  
 CC FT ACT\_SITE 196 196 BY SIMILARITY.  
 CC SEQUENCE 272 AA: 30168 MW: 77DD0917FD12FDFR CRC64:

Query Match 37.8%; Score 215; DB 10; Length 272;  
 Best Local Similarity 48.0%; Pred. No. 6.2e-15;  
 Matches 48; Conservative 14; Mismatches 34; Indels 4; Gaps 1;

QY 4 DSFVKTEAFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISEA 63  
 DB 176 DSDRYRSARFLLAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISGCI 231  
 QY 64 HNAKNGALPKPELVDAKGTWIVLRVDEINRDVALIKYV 103  
 DB 232 KRAVKVISPPLNLSNGEDPMWTVTRVDEIKPIYALLNFGSLTV 271

## RESULT 10

Q9S9E4 PRELIMINARY: PRT: 258 AA.  
 ID Q9S9E4  
 AC Q9S9E4;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE RNA -glycosidase (EC 3.2.2.22).  
 OS Gelonium multiflorum (Euphorbiaceae himalaya).  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots; Rosidae;  
 OC eucosids I; Malpighiales; Euphorbiaceae; Gelonium.  
 RX NCBI\_TaxID=3979;  
 RN (1)  
 RP SEQUENCE.  
 RC MEDLINE=96006751; Pubmed=7553224;  
 RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,  
 RA Toman P.D., Cheung L.;  
 RT "Amino acid sequence analysis, gene construction, cloning, and  
 RT expression of gelonin, a toxin derived from Gelonium multiflorum.";  
 RL J. Interferon Cytokine Res. 15:547-555(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC HSSP: P09989; IMRI.  
 CC DR InterPro: IPR001574; RIP.  
 CC Pfam: PF00161; RIP; 1.  
 CC DR PRINTS: PR00396; SHIGARICIN.  
 CC KW Hydrolase; Toxin.  
 CC SEQUENCE 258 AA: 28826 MW: 13D68E673F4D6B06 CRC64:

Query Match 37.3%; Score 212.5; DB 10; Length 258;  
 Best Local Similarity 44.7%; Pred. No. 1.1e-14;  
 Matches 46; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 3 VDSFVKTEAFLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISEA 62  
 DB 152 IDNKRPTIASLLVAIONVSEARFKYIENQVNTFNRAFPDPKVINLEKMGKISFQ 211  
 QY 63 IHNKNGALPKPELVDAKGTWIVLRVDEINRDVALIKYV 104  
 DB 212 IRTSGANGMFEAEVLERANGKRYVAVDQVKPKIKALKRVD 254

## RESULT 11

Q9M5K6 PRELIMINARY: PRT: 279 AA.  
 ID Q9M5K6  
 AC Q9M5K6;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE RNA -glycosidase (EC 3.2.2.22).  
 GN CAP30A.  
 OS Chenopodium album (lamb's-quarters).  
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots;  
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.  
 RX NCBI\_TaxID=3559;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC "A cDNA clone encoding a novel ribosome inactivating protein from  
 RT Chenopodium album L.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC EMBL: AF228508; AAF6234.1; .  
 CC DR HSSP: Q03464; IAPA.  
 CC DR InterPro: IPR001574; RIP.  
 CC Pfam: PF00161; RIP; 1.  
 CC DR PRINTS: PR00396; SHIGARICIN.  
 CC KW Hydrolase; Toxin.  
 CC SEQUENCE 279 AA: 31377 MW: 2A5330E445DC952 CRC64:

	Query Match	Similarity	47.4%	Pred.	No. 4,1e-14;	Mismatches	46;	Conservative	15;	Gaps	2
DQ	KTEAFFLLVAIOMSEARFKYIENQ--VKTNFNRAFPDPKVINLEEKWKISEAIIHNA	9		:	:  ::  ::  ::  :	:		:	:	:	:
Dd	KTEAFREFLIAIQWAEARFYGIRATIVTTAPN-----DKILSLNNMGALSKGIRNA	187									241
OY	KGNGALPKLPLVDAKGTWIYLRLNDVALLKRY	67	:	:	:	:	:	:	:	:	103
Dd	VKKVINPEITLOYPDGKWIVTGVSDVKNDMLTKRV	242									278
<hr/>											
	RESULT 12										
ID	09AUJ3	PRELIMINARY:	PRT;        279 AA.								
AC	09AUJ3:										
DT	01-JUN-2001 (TREMBLrel .17, Created)										
DR	01-JUN-2001 (TREMBLrel .17, Last sequence update)										
DE	01-MAR-2002 (TREMBLrel .20, Last annotation update)										
CX	rRNA_glycosidase (EC 3.2.2.22).										
CC	CAP30B:										
OS	Chenopodium album ('lamb's-quarters').										
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;										
SC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;										
CC	Caryophyllales; Caryophyllaceae; Chenopodiaceae; Chenopodum.										
NCHI_TaxID=3559;											
RN	[1]										
RP	SEQUENCE FROM N.A.										
PA	Park J.S., Lee S.M., Kim Y.T., Cho K.J.;										
RT	"Molecular characterization of a new cDNA clone encoding a ribosome-										
LT	inactivating protein (CAP30B) from Chenopidium album."										
RU	Submitted (Feb-2000) to the EMBL/Genebank/DDJJ databases.										
CC	- I - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 2BS RNA.										
CC	- I - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.										
DR	EMBL: AF230812; AAK28323.1; ..										
DR	HSSP: Q03464; IAPA.										
DR	InterPro: IPRO01574; RIP.										
PIam:	PF00161; RIP; 1.										
DR PRINTS:	PRO0396; SHIGARTCN.										
KM Hydrolase; Toxin.											
SO SEQUENCE	279 AA; 31419 MW; 97E934FE2C8033AF CRC64;										
<hr/>											
	Query Match	Similarity	34.7%	Score	197.5;	DB 10;	Length	279;			
	Best Local Similarity	45.4%;	Freq.	No. 4,8e-13;							
	Matches	44;	Conservative	17;	Mismatches	29;	Indels	7;	Gaps	2	
OY	KTEAFFLLVAIOMSEARFYIENO-VKTNFNRAFPPDVINLEEKWKISEAIIHNA	9	::::	:	:  ::  ::  ::  :	:		:	:	:	
Dd	KTEAREFLIAIQWAEARFYIOGRAIVTTAPN-----NKYISLETNMGALSIGIRNA	187								241	
OY	KGNGALPKLPLVDAGTWIYLRLNDDVALLKRY	67	:	:	:	:	:	:	:	:	
Dd	VKKVINPEITLOYPDGKITVIOTVSADVKNMDGLTKRV	242								278	
<hr/>											
	RESULT 13										
ID	041174	PRELIMINARY:	PRT;        541 AA.								
AC	041174:										
DT	01-NOV-1996 (TREMBLrel .01, Created)										
DR	01-NOV-1996 (TREMBLrel .01, last sequence update)										
DE	01-JUN-2002 (TREMBLrel .21, last annotation update)										
CX	rRNA_glycosidase (EC 3.2.2.22) (Fragment).										
OS	Ricinus communis (Castor bean).										
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;										
SC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;										
CC	eurosidia II; Malpighiales; Euphorbiaceae; Ricinus.										
NCHI_TaxID=3988;											
RN	[1]										
RP	SEQUENCE FROM N.A.										

RX	MEDLINE=92338377; PubMed=1633311
RA	Roberts L.M., Tiegear J.W., Lord J.M.:
RT	"Molecular cloning of Ricin."
RL	Targeted Diagn. Ther. 7:81-97(1992).
CC	-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RNA.
CC	-I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR	EMBL: S40366; AB22582.1; -.
DR	HSSP: P02879; 1BR6.
DR	InterPro: IPR000772; Ricin_B_lectin.
DR	InterPro: IPR001574; RIP.
DR	InterPro: IPR001400; Somatostatin.
DR	Pfam: PF00652; Ricin_B_lectin; 6.
DR	Pfam: PF00161; RIP; 1.
DR	PRINTS: PR00396; SHIGARICIN.
DR	SMART: SM00458; RICIN; 2.
DR	PROSITE: PS50231; RICIN_B_LECTIN; 2.
DR	PROSITE: PS00275; SHIGA_RICIN; 1.
DR	PROSITE: PS00338; SOMATOTROPIN_2; UNKNOWN_1.
KW	Hydrolase; Toxin.
FT	NON_TER
SQ	SEQUENCE 541 AA: 60281 MW; 287B2CDEF1F2E9D9 CRC64;
Query Match	33.7%; Score 192; DB 10; Length 541;
Best Local Similarity	39.8%; Pred. No. 4.3e-12;
Matches 41: Conservative	19; Mismatches 39; Indels 4; Gaps 2
OY	2 GVDSFPVTEAFFLVAIQMSSEARFYIEINVKT--NFNRAFPPDKVINLEEKWKGI 59
Db	157 GGTLQPLTARSF--ITCIQMISEARFPIEGEMTRIRYNRSAPDDSVITLNSMGRL 214
OY	60 SEAIHNAKNGALPKPLELDVDAKGTWIVLRDEINRDVALKY 102
Db	215 STAOESNOGAFASPIQLQRNRGSKEFSYDVASILPIALMY 257
RESULT 14	
ID	Q8W4U4 PRELIMINARY; PRT: 305 AA.
AC	Q8W4U4.
DT	01-MAR-2002 (TREMBLrel. 20; Created)
DT	01-MAR-2002 (TREMBLrel. 20; Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21; Last annotation update)
DE	Bouganlin.
OS	Bougainvillea spectabilis.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Caryophyllidae; Caryophyllales; Nyctaginaceae; Bougainvillea.
OX	NCBI_TaxID=146096;
RP	(1)
SP	SEQUENCE FROM N.A.
RA	den Hartog M.T., Lubelli C., Boon L., Heerkens S., Ortiz Bujsse A.P.,
RA	de Boer W., Stijpe F.;
RT	"Cloning and expression of cDNA coding for bouganlin: A type I
RL	ribosome-inactivating protein from Bougainvillea spectabilis Willd.";
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF454516; AAL35962.1; -.
DR	InterPro: IPR001574; RIP.
DR	Pfam: PF00161; RIP; 1.
DR	PRINTS: PR00396; SHIGARICIN.
DR	PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
DR	PROSITE: PS00275; SHIGA_RICIN; UNKNOWN_1.
SQ	SEQUENCE 305 AA: 34067 MW; 31505CE91962DCB8 CRC64;
Query Match	33.1%; Score 188.5; DB 10; Length 305;
Best Local Similarity	43.6%; Pred. No. 5e-12;
Matches 41: Conservative	18; Mismatches 32; Indels 3; Gaps 2
OY	12 AFFLVLAIQMSSEARFYIEINV-KTNFNNAFYDDPVINMLEEKWKITSEAIHNA--KN 68
Db	179 AKFLVLVIQMSSEARFYIEITVEVDRDLVSFKRNPFLVNLENMWGDLSDAIHSSPOC 238
OY	69 GALPKPLELDVDAGKTWIVLRDEINRDVALKY 102

Db 239 TTINPALQLSPSNDPWWNVKVSQISPDGILKF 272

## RESULT 15

Q93Y65  
ID Q93Y65 PRELIMINARY; PRT; 294 AA.  
AC Q93Y65;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE rRNA-glycosidase (EC 3.2.2.22).  
OS Dianthus chinensis.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.  
OX NCBI\_TaxID=118431;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20306826; Pubmed=10850653;  
RA Cho H.J., Lee S.J., Kim S., Kim B.D.;  
RT Isolation and characterization of cDNAs encoding ribosome  
RT inactivating protein from Dianthus sinensis L.;  
RL Mol. Cells 10:135-141(2000).  
CC -!- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
CC EMBL: AF219237; AK68928.1; -  
DR InterPro: IPR001574; RIP.  
DR Pfam: PF00161; RIP; 1.  
KW Hydrolase; Toxin.  
SQ SEQUENCE 294 AA; 3331 MW; 659E72DD847A72D0 CRC64;

Query Match 30.0%; Score 170.5; DB 10; Length 294;  
Best Local Similarity 55.2%; Pred. No. 4e-10;  
Matches 37; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 8 VKTEAFFLLVAIQWSEARFKYIENOVKTNFRAFYDDPKYINLEEKWKISEAITH-NA 66  
DB 185 VKDEARFLLIGIQMSAEAVFRFIQNLVTRNPFKFNKSDNTVIQYOTSMGKISEAITHDC 244  
QY 67 KNGCALPK 73  
DB 245 KNGKFNK 251

Search completed: July 2, 2003, 11:42:10  
Job time : 15.912 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 38.04 Seconds  
(Without alignments)  
1424.413 Million cell updates/sec

Title: US-09-978-274A-4

Perfect score: 1357  
Sequence: 1 MINTTFDAGNATINKYATF.....DEINRDVALIKYVNGTCQTT 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	1352	99.6	314	10 P93444	P93444 phytoiaacca
2	1332	98.2	262	10 O8S946	O8S946 phytoiaacca
3	1099.5	81.0	261	10 O8S947	O8S947 phytoiaacca
4	1044	72.0	313	10 O941G8	O941G8 phytoiaacca
5	977.5	72.0	315	10 O9XFF8	O9XFF8 phytoiaacca
6	965	71.1	339	10 O8RYA4	O8RYA4 phytoiaacca
7	953	70.2	237	10 O8RYB3	O8RYB3 phytoiaacca
8	701	51.7	302	10 P93077	P93077 phytoiaacca
9	425.5	31.4	289	10 P93261	P93261 phytoiaacca
10	395	29.1	279	10 O9MSK6	O9MSK6 chenopodium
11	394	29.0	272	10 O394I8	O394I8 beta vulgar
12	382	28.2	279	10 O9AUE3	O9AUE3 chenopodium
13	328	24.2	294	10 O93Y65	O93Y65 dianthus ch
14	328	24.2	294	10 O93Y64	O93Y64 dianthus ch
15	321.5	23.7	258	10 O9S9E4	O9S9E4 geilonium mu
16	315	23.2	294	10 O93Y66	O93Y66 dianthus ch

17	301	22.2	305	10 O8W404	O8W404 bougainvill
18	292	21.5	541	10 O41174	O41174 ricinus com
19	287	21.1	319	10 O8WY2	O8WY2 spinacia ol
20	258.5	19.0	279	10 O9ZT25	O9ZT25 amarantus
21	248.5	18.3	251	10 O48859	O48859 amarantus
22	243	17.9	278	10 O00980	O00980 luffa cylin
23	242	17.8	289	10 O94KE4	O94KE4 trichosan
24	241	17.8	247	10 O9LRE3	O9LRE3 trichosan
25	239	17.6	270	10 O41611	O41611 trichosan
26	237	17.5	270	10 O9SA05	O9SA05 amarantus
27	236	17.4	580	10 O94BW3	O94BW3 cinamomum
28	235	17.3	289	10 O94B16	O94B16 trichosan
29	234	17.2	284	10 O96322	O96322 amarantus
30	234	17.2	581	10 O94BW5	O94BW5 cinamomum
31	234	17.2	604	10 O9M654	O9M654 polygonatum
32	233.5	17.2	563	10 O94552	O94552 sambucus ni
33	231.5	17.1	566	10 O04072	O04072 sambucus ni
34	231	17.0	580	10 O94BW4	O94BW4 cinamomum
35	230.5	17.0	252	10 O38761	O38761 abrus preca
36	228	16.8	549	10 O9FV22	O9FV22 cinamomum
37	226.5	16.7	547	10 O9M6E9	O9M6E9 abrus preca
38	226	16.7	565	10 O04071	O04071 sambucus ni
39	224.5	16.5	251	10 O96236	O96236 abrus preca
40	223.5	16.5	251	10 O96237	O96237 abrus preca
41	221.5	16.3	573	10 O8W2E8	O8W2E8 iris hollan
42	219.5	16.2	592	10 O8W2E7	O8W2E7 iris hollan
43	217.5	16.0	251	10 O96235	O96235 abrus preca
44	217.5	16.0	252	10 O38760	O38760 abrus preca
45	216.5	16.0	603	10 O9M653	O9M653 polygonatum

## ALIGNMENTS

RESULT 1  
ID P93444 PRELIMINARY: PRT: 314 AA.  
AC P93444;  
AD 01-MAY-1997 (TREMUREL. 03, Created)  
DT 01-MAY-1997 (TREMUREL. 03, Last sequence update)  
DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)  
DE rRNA - glycosidase precursor (EC 3.2.2.22).  
DE PAP-S.  
OS Phytoiaacca americana (Common pokeweed) (Virginian pokeweed).  
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
OC Caryophyllidae: Caryophyllales: Phytoiaaccaceae: Phytoiaacca.  
OX NCBI\_taxid=3527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SEED.  
RX MEDLINE=97263479; PubMed=9109394;  
RA Poyet J. L., Hoeveler A.;  
RT "CDNA cloning of the gene encoding the Antiviral Protein from the  
RT seeds of Phytoiaacca americana and its expression in E. coli.";  
RL FEBS Lett. 406:97-100(1997).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
CC EMBL: X98079; CA66702.1; -;  
CC DR HSSP: O03464; IAPA.  
CC DR InterPro: IPR001574; RIP.  
CC DR Pfam: PF00161; RIP; 1.  
CC DR PRINTS: PR00396; SHIGARICIN.  
CC DR PROSITE: PS00275; SHIGA\_RICIN; 1.  
CC KW Hydrolyase; Signal; Toxin.  
CC FT SIGNAL: 1 24 POTENTIAL.  
CC FT CHAIN: 25 314 POTENTIAL.  
CC SQ SEQUENCE 314 AA: 35323 MW: A8963CE57789FF9E CRC64;  
Query Match 99.6%; Score 1352; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 3.2e-105;  
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGLOGANLK 61
DB 25 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGLOGANLK 84
QY 62 TITLMLRRNNLYMGVSDPENGKCRHYHFNDDITSTERTVENTLCCSSSSSRVAMSINTYN 121
DB 85 TITLMLRRNNLYMGVSDPENGKCRHYHFNDDITSTERTVENTLCCSSSSSRVAMSINTYN 144
QY 122 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDSFPVKTEAFLLVAIQWSEAAAF 181
DB 145 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDSFPVKTEAFLLVAIQWSEAAAF 204
QY 182 KYIENOVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIVL 241
DB 205 KYIENOVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIVL 264
QY 242 RVDEINRDVALLKYVNGTCOTT 263
DB 265 RVDEINRDVALLKYVNGTCOTT 286

RESULT 2
QY 08S946 PRELIMINARY: PRT: 262 AA.
AC 08S946:
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE PAP-S2 (Fragment).
GN PAP-S2.
OS Eukaryota americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Honjo E., Matanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB071855; BAB86350.1; -
FT NON_TER 1 1
FT SEQUENCE 262 AA: 29486 MW: AF2D010A73C9D18B CRC64;

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Query Match 98.2%; Score 1332; DB 10: Length 262;
Best Local Similarity 98.1%; Pred. No. 1.2e-103;
Matches 257; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGLOGANLK 61
DB 1 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGLOGANLK 60
QY 62 TITLMLRRNNLYMGVSDPENGKCRHYHFNDDITSTERTVENTLCCSSSSSRVAMSINTYN 121
DB 61 TITLMLRRNNLYMGVSDPENGKCRHYHFNDDITSTERTVENTLCCSSSSSRVAMSINTYN 120
QY 122 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDSFPVKTEAFLLVAIQWSEAAAF 181
DB 121 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDSFPVKTEAFLLVAIQWSEAAAF 180
QY 182 KYIENOVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIVL 241
DB 181 KYIENOVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIVL 240
QY 242 RVDEINRDVALLKYVNGTCOTT 263
DB 241 RVDEINRDVALLKYVNGTCOTT 262

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RESULT 3
QY 08S947 PRELIMINARY: PRT: 261 AA.
AC 08S947:
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE PAP-S1 (Fragment).
GN PAP-S1.
OS Eukaryota americana (Common pokeweed) (Virginian pokeweed).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.
OX NCBI_TaxID=3527;
RN [1]
RP SEQUENCE FROM N.A.
RA Honjo E., Matanabe K.;
RT "Cloning of genomic DNA encoding two types of pokeweed antiviral
RT protein in seeds, PAP-S1 and PAP-S2, and functional comparison of
RT their recombinant proteins with other PAP isoforms."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB071854; BAB86349.1; -
FT NON_TER 1 1
FT SEQUENCE 261 AA: 29199 MW: D8BB98BEEF1F989 CRC64;

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Query Match 81.0%; Score 1099.5; DB 10: Length 261;
Best Local Similarity 83.2%; Pred. No. 3.5e-84;
Matches 218; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGLOGANLK 61
DB 1 INTTFDAGNATINKYATFEMESLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGLOGANLK 60
QY 62 TITLMLRRNNLYMGVSDPENGKCRHYHFNDDITSTERTVENTLCCSSSSSRVAMSINTYN 121
DB 61 TITLMLRRNNLYMGVSDPENGKCRHYHFNDDITSTERTVENTLCCSSSSSRVAMSINTYN 119
QY 122 SLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDSFPVKTEAFLLVAIQWSEAAAF 181
DB 120 GLVPTMEKKAENVSRNOVQGIOLSSDICKISGVDSFPVKTEAFLLVAIQWSEAAAF 179
QY 182 KYIENOVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIVL 241
DB 180 KYIENOVKTNFNRAFPDPKVINLEEKMGKISEAHNNAKNGALPKPLEVDAGTKWIVL 239
QY 242 RVDEINRDVALLKYVNGTCOTT 263
DB 240 RVDEINRDVALLKYVNGTCOTT 261

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RESULT 4
QY 0941G8 PRELIMINARY: PRT: 313 AA.
AC 0941G8:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE rRNA - 24S ribosomal RNA (EC 3.2.2.22).
GN PAP.
OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Caryophyllales: Caryophyllales: Phytolaccaceae: Phytolacca.
OX NCBI_TaxID=107615;
RN [1]
RP SEQUENCE FROM N.A.
RA Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.
DR EMBL: AY049785; AAL15442.1; -

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DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 KW Hydrolase: Toxin.  
 SQ SEQUENCE 313 AA: 35059 MW: 6478ECD571C17885 CRC64:

Query Match 76.9%; Score 1044; DB 10; Length 313;  
 Best Local Similarity 76.0%; Pred. No. 2e-79;  
 Matches 199; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

OY 2 INTTFDAGNNTINKYATFMESLRNQAQDKPKLKCIGIMLPDNTSTPKYLLVAGALNK 61  
 DB 23 VNTIYVNGSTTSTYATFELDLNLRKADPSLCKGIMLPNTNPKYVLEVLQSSNKK 82  
 OY 62 TITLMLRRNNLYVNGSDPFGNKKRYHIFNDITSTERTDVENTLCSSSSSRVAMSYN 121  
 DB 83 TITLMLRRNNLYVNGSDPFGTNCRCYHIFSDISTGTEODVETTLCPNPNRSVKNINYD 142  
 OY 122 SLVPTMEKAEVNSRNOVQGIQLSSDICKISGVDSFPVKTEAFELVIAIOMVSEARF 181  
 DB 143 SRYPTLESKAGVSKSRQVQLGILDSNIGKISGVSTFTEKTEAEFLVIAIOMVSEARF 202  
 OY 182 KYIENQVKTNNRAFYDPKVINLEEKWKGISFAIHAKNGALPKPLVDAKGTWIVL 241  
 DB 203 KYIGQVKTNNRAFNPNPKVNLNEETWKGISTAIHDKNGLPKPLVDASGAKWIVL 262  
 OY 242 RVDEINRDVALLKVYNGTCQTT 263  
 DB 263 RVDEIKRPDVALNLYVNGSCQTT 284

RESULT 5  
 O9XFF8 PRELIMINARY: PRT: 315 AA.

AC O9XFF8: 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22).  
 GN PIP2.  
 OS Phytolacca insularis.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC NCB1\_TaxID=63144;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20505377; PubMed=11052196;  
 RA Song S.-K., Choi Y., Moon Y.-H., Kim S.-G., Choi Y.-D., Lee J.-S.;  
 RT "Systemic induction of a Phytolacca insularis antiviral protein gene  
 by mechanical wounding, jasmonic acid, and abscisic acid.";  
 RL Plant Mol. Biol. 43:439-450(2000).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC EMBL: AF141331; AAD32679.1; -  
 DR HSSP: Q03464; IAPA.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR000396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN; UNKNOWN\_1.  
 KW Hydrolase: Toxin.  
 SQ SEQUENCE 315 AA: 35728 MW: F85DE21154B5FA15 CRC64;

Query Match 72.0%; Score 977.5; DB 10; Length 315;  
 Best Local Similarity 74.0%; Pred. No. 7.3e-74;  
 Matches 194; Conservative 28; Mismatches 37; Indels 3; Gaps 3;

OY 3 NTTFDAGNATINKYATFMESLRNQAQDKPKLKCIGIMLPDNTSTPKYLLVAGALNK 62  
 DB 28 NPITFEVGNATINKATFMESLRNQAQDKPKLKCIGIMLPDNTSTPKYLLVAGALNK 87  
 OY 63 ITLMLRRNNLYVNGSDPFGNKKRYHIFNDIT-STERTDVENTLCSSSSSRVAMSYN 121  
 DB 263 RVDEIKRPDVALNLYVNGSCQTT 284

DB 88 ITLMLRRNNLYVNGYADTYN-NKCRHYIFKDISNTTERNDVMTLCPNMSSRVKKNISYD 146  
 OY 122 SLVPTMEKAEVNSRNOVQGIQLSSDICKISGVDSFPVKTEAFELVIAIOMVSEARF 181  
 DB 147 SSYPALEKKGK-RRSKQVQLGILDSNIGKISGVSTFTEKTEAEFLVIAIOMVSEARF 205  
 OY 182 KYIENQVKTNNRAFYDPKVINLEEKWKGISFAIHAKNGALPKPLVDAKGTWIVL 241  
 DB 206 KYIENQVKTNNRAFNPNPKVNLNEETWKGISTAIHDKNGLPKPLVDASGAKWIVL 265  
 OY 242 RVDEINRDVALLKVYNGTCQTT 263  
 DB 266 RVDEIKRPDVALNLYVNGTCQTT 287

## RESULT 6

O8RYA4 PRELIMINARY: PRT: 339 AA.  
 AC O8RYA4: 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Ribosome inactivating protein type 1 precursor.  
 OS Phytolacca americana (Common pokeweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Phytolaccaceae; Phytolacca.  
 NCBI\_TaxID=3527;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Park S.-W., Lawrence C.B., Linden J.C., Vivanco J.M.;  
 RT "Characterization of a novel ethylene-inducible ribosome-inactivating  
 protein exuded from root cultures of Phytolacca americana.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY071928; AAL61546.1; -  
 KW Signal.  
 FT SIGNAL  
 SQ SEQUENCE 339 AA: 37978 MW: 7D47BDC2DED965F CRC64;

Query Match 71.1%; Score 965; DB 10; Length 339;  
 Best Local Similarity 72.4%; Pred. No. 8.9e-73;  
 Matches 189; Conservative 22; Mismatches 46; Indels 4; Gaps 1;

OY 5 ITFDAGNATINKYATFMESLRNQAQDKPKLKCIGIMLPDNTSTPKYLLV----KLGANL 60  
 DB 49 ISFDVGSATISKYTTFOESLRNQAQDKPKLKCIGIMLPDNTSTPKYLLVSEV 108  
 OY 61 KTTLMLRRNNLYVNGYSDPFGNKKRYHIFNDITSTERTDVENTLCSSSSSRVAMSYN 120  
 DB 109 KTTLMLRRNNLYVNGYSDPIDVKKCRFHTEKDISGTERQVETTLCPDPSRIKDIY 168  
 OY 121 NSLPTMEKAEVNSRNOVQGIQLSSDICKISGVDSFPVKTEAFELVIAIOMVSEAR 180  
 DB 169 DSRYPTEMTKAGVSGSOVQGLIELNSGICKISGVSTFTEKTEAEFLVIAIOMVSEAR 228  
 OY 181 FKYEIENQVKTNNRAFYDPKVINLEEKWKGISFAIHAKNGALPKPLVDAGKTWIVL 240  
 DB 229 FKYEIENQVKTNNRAFGFPDPKVISLEEKWKGISFAIHAKNGALPKPLVDAGKTWIVL 288  
 OY 241 RVDEINRDVALLKVYNGTCQ 261  
 DB 289 RVDEIKSDVGLKLVYTGSCQ 309

RESULT 7  
 O9ATB3 PRELIMINARY: PRT: 237 AA.

AC O9ATB3: 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22) (Fragment).  
 GN MPAP.



OS Phytolacca americana (Common pokeberry) (Virginian pokeweed).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 OC Caryophyllidae: Caryophyllales: Phytolaccaceae: Phytolacca.  
 NCBI\_TaxID=3537;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chen D., Wang X., Zhou G.;  
 RT "Pokeweed antiviral protein gene/partical cds.";  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: AF338910; AAK21951.1; -.  
 DR HSSP: P10297; 10CG.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN: 1.  
 KW Hydrolyase; toxin.  
 FT NON\_TER 1  
 FT TER 237  
 SQ SEQUENCE 237 AA; 26534 MM; FE4ADCE03464783 CRC64;  
 Query Match 70.2%; Score 953; DB 10; Length 237;  
 Best Local Similarity 75.9%; Pred. No. 5.7e-72;  
 Matches 180; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 2 ITTFDGNATINKYATFMESLRNQAOKPKLCYGIPLPDTNTPKYLKLOGANLTK 61  
 DB 1 VNTIITNGSTTISKYATFLNDLRNKAOKPSLCKYGIPLPDTNTPKYLKLOGSNKK 60

QY 62 TITLMLRNLLVYMGSDPFNGNCRHYIFNDITSTERTDVNTLCSSSSSRVAMSINYN 121  
 DB 61 TITLMLRNLLVYMGSDPFNGNCRHYIFNDITSTERTDVNTLCPSRANSRVSKNINFD 120

QY 122 SLVFTMEKKAVERNNOVQLOIQLSSDICKISGVDSFVPTAEFLLVAIQMSEARF 181  
 DB 121 SRYPTLESKAGVRSQVQLOIQLSDNIGKISGVMSFTEKTEAEFLVAIQMSEARF 180

QY 182 KYINOVKTNRNKAFYDPKVINLEEMKQISEAIIHNKAKLPRKPLELVAKGKW 238  
 DB 181 KYINOVKTNRNKAFNPKVNLQETWKGISTAIHGAKNGVLPKPLELVDSAGKW 237

RESULT 8  
 P93077 PRELIMINARY: PRT: 302 AA.  
 AC P93077;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 GN CN  
 OS Clerodendrum aculeatum  
 CC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 CC Asteridae: euasterids I; Lamiales: Lamiales: Clerodendrum.  
 CC NCBI\_TaxID=54208;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-LEAF;  
 MEDLINE=97238481; PubMed=9132066;  
 RA Kumar D., Verma H.N., Tuteja N., Tewari K.K.;  
 RT "Cloning and characterisation of a gene encoding an antiviral protein  
 from Clerodendrum aculeatum L.";  
 RL Plant Mol. Biol. 33:745-751(1997).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: X96474; CA665328.1; -.  
 DR EMBL: X96583; CA65402.1; -.  
 DR HSSP: P10297; 10CG.

DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 DR PROSITE: PS00275; SHIGA\_RICIN: 1.  
 KW Glycosidase; Hydrolyase; Toxin.  
 SQ SEQUENCE 302 AA; 33955 MM; B0561C3918C2E6A2 CRC64;  
 Query Match 51.7%; Score 701; DB 10; Length 302;  
 Best Local Similarity 56.1%; Pred. No. 9.7e-51;  
 Matches 143; Conservative 31; Mismatches 79; Indels 2; Gaps 2;

QY 7 FDAGNATINKYATFMESLRNQAOKPKLCYGIPLPDTNTPKYLKLOGANLTKITLM 66  
 DB 30 FHVGATISITTEINTLRNKAOKPSLCKYGIPLPPTTQPKVLRRLDADAATTITLI 89

QY 67 LRNNLLVYMGSDPFNGNCRHYIFNDITSTERTDVNTLCSSSSSRVAMSINNSLYPT 126  
 DB 90 YNRITNLVYLGSDPFNG-ECRHYIFSDYRGTDREAVDTLCPDRENRVQKIDINESNOS 148

QY 127 MEKKAVERNNOVQLOIQLSSDICKISGVDSFVPTAEFLLVAIQMSEARFXYEN 186  
 DB 149 MENKAG-KSRAQLDELGINILKSSIEKISGVRAFTKEVEAEFLVAIQMTEAARXYEN 207

QY 187 QVKTENRRAFYPDPKVINLEEMKQISEAIIHNKANGALPKLELVDAKGTWYLRDEI 246  
 DB 208 LVKTNFNENFKPDHKMLRELTLTWGKISTPIRMAONGVISPLNLNSSGEDPFWVTRDEI 267

QY 247 NRVALALKYVNGTQ 261  
 DB 268 KPYIALNLFNGTQ 282

RESULT 9  
 P93261 PRELIMINARY: PRT: 289 AA.  
 AC P93261;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE rRNA - glycosidase (EC 3.2.2.22).  
 GN CN  
 OS Mesembryanthemum crystallinum (Common ice plant).  
 CC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:  
 CC Caryophyllidae: Caryophyllales: Alzooceae: Mesembryanthemum.  
 CC NCBI\_TaxID=3544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98087998; PubMed=9426592;  
 RA Rippmann J.F., Michalowski C.B., Nelson D.E., Bohnert H.J.;  
 RT "Induction of a ribosome-inactivating protein upon environmental  
 stress.";  
 RL Plant Mol. Biol. 35:701-709(1997).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 DR EMBL: U80072; AAB96824.1; -.  
 DR HSSP: P10297; 10CG.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PR00396; SHIGARICIN.  
 KW Glycosidase; Hydrolyase; Toxin.  
 SQ SEQUENCE 289 AA; 32652 MM; 132AA996FBA27FID CRC64;  
 Query Match 31.4%; Score 425.5; DB 10; Length 289;  
 Best Local Similarity 39.1%; Pred. No. 1.1e-27;  
 Matches 100; Conservative 44; Mismatches 105; Indels 7; Gaps 4;

QY 4 TTFDAGNATINKYATFMESLRNQAOKPKLCYGIPLPDTNTPKYLKLOGANLTKI 63  
 DB 23 TLVLDIGATGTEKTSDDMTKLRIFAKGKDMYVGLSMMPKPTKPTLYLVAIAKSKMSI 82

QY 64 TLMRLNNLLVYMGSDPFNGNCRHYIFNDITSTERTDVNTLCSSSSSRVAMSINNSL 123

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Db      83 TLSLSRDLVVGISDMYK-KCRYHVEPHDSKPPYECHSLCDKAKDAIRKPIGVSS 141
QY      124 YPTMEKKAEVNSRNOVLOGIOLSSDICKISGVDFPVKTEAFELVLAIOVSPARFKY 183
      142 YTELERAKARKNKEIGLGVNKLTLIPKYYGSESKYQDEAFELVLAITITAEARFPY 201
QY      184 IENOVKTENRAFYPPPKVINLEEKWKCKISEAIIHNAKNGALPPLELVDAKGTWIVLRY 243
      202 IEKIAETAAAN----PDOTAICLENMNSKISKETIYNQKGNPQTPAKDVATVTCCK-NLKG1 256
Db      244 DEINRDVALLKYNGT 259
QY      257 NOVOKYITLLSY-OGT 271

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## RESULT 10

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Q9M5K6 PRELIMINARY; PRT; 279 AA.
AC Q9M5K6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE rRNA - glycosidase (EC 3.2.2.22).
GN CAP30A.
OS Chenopodium album (Lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiales; Chenopodium.
OX NCBI_TaxID=3559.
RN [1]
RP SEQUENCE FROM N.A.
RA Park J.S., Cho K.J., Lee S.M., Kim Y.T., Hwang Y.S.;
RT "A cDNA clone encoding a novel ribosome inactivating protein from
RT Chenopodium album L."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
DR EMBL: AF228508; AAF6234.1; -.
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHIGARICIN.
DR HydroLase; Toxin.
SQ SEQUENCE 279 AA: 31377 MW; 2A53300E445DC952 CRC64;

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Query Match 29.1%; Score 395; DB 10; Length 279;

Best Local Similarity 40.1%; Pred. No. 3.6e-25; Matches 101; Conservative 37; Mismatches 96; Indels 18; Gaps 8;

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QY      13 TINKYATFESLBNQAKDPKLCYGIPLPDTNSTPKYLLVKGQ---NLKTTMLLR 69
      37 TONTYTFIQSINQAKDPSLYEGIPMIRAPTNPTIILVELSKKNNEISITLALSR 96
QY      70 NNLVYGVSDPENGKCRHYIFNDITSTERTDVENTLCCSSSSRVAMSIYNVSLYPTMEK 129
      97 NDLVYVAADKF-GKVRGHYFKNL-GISTDEANKVFPVQDFI--NITYGSYNQIES 152
Db      130 KAEVNSRNOVLOGIOLSSDICKISGVDFP---VTEAFELVLAIOVSEARFYIEN 186
      153 NGNTN-RLSEFPLGFDLTKYSRNKVVYGMDDTTGGYSTEARFLIAIOWVAEARFYIOG 211
QY      187 Q--VKTNFRARFYPDPKVINLEEKWKCKISEAIIHNAKNGALPKPLELVDAKGTWIVLRY 244
      212 RAIVTTAPN-----DKIITSLNMGALSKGINNAKKVYIPPTITLOYPDGKFWIVTQVS 266
QY      245 EINRDVALLKYV 256
      267 DVKNDMGILLKYV 278
Db

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## RESULT 11

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Q39418 PRELIMINARY; PRT; 272 AA.
AC Q39418;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Antiviral protein precursor (Ribosome-inactivating protein) (RRNA N-
DE glycosidase) (Polynucleotide:adenosine glycosidase) (EC 3.2.2.22)
DE (BETAVULGIN) (BVG).
GN RIP OR BETAVULGIN OR BVG.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiales; Beta.
OX NCBI_TaxID=3555.
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RC TISSUE-SEEDLING;
RX MEDLINE=96235141; PubMed=8666251;
RA Horning E., Majant H., Jeske H., Mundry K.-W.;
RT "Cloning of a cDNA encoding a new ribosome-inactivating protein from
RT Beta vulgaris vulgaris (mangold).";
RL Gene 170:233-236(1996).
CC -1- FUNCTION: INHIBITS VIRAL INFECTION OF PLANTS. AND PROTEIN
CC SYNTHESIS IN VITRO. THE PROTEIN MAY PROVIDE A MEANS OF CELLULAR
CC SUICIDE UPON INVASION BY A VIRUS.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
CC PROTEINS.
CC -1- SIMILARITY: BELONGS TO TYPE 1 RIP.
DR EMBL: X85967; CAAS9952.1; -.
DR HSSP: Q03464; IAPA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.1.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA-RICIN; FALSE_NEG.
KW HydroLase; Glycosidase; Antiviral; Protein synthesis inhibitor; Toxin;
KW Multigene family; Signal.
FT SIGNAL 1 23
FT CHAIN 24 272 ANTIVIRAL PROTEIN.
FT ACT_SITE 196 196 BY SIMILARITY.
FT ACT_SITE 196 196
SQ SEQUENCE 272 AA: 30168 MW; 77DD0917FD12DFDF CRC64;

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Query Match 29.0%; Score 394; DB 10; Length 272;

Best Local Similarity 40.5%; Pred. No. 4.2e-25; Matches 105; Conservative 36; Mismatches 98; Indels 20; Gaps 7;

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QY      5 IFPDAGNATINKYATFESLBNQAKDPKLCYGIPLPDTNSTPKYLLVKGQ---GANL 60
      26 VTFDELTAASKTKCTFLSNRNINVKOSKLYBEDIPMIRAPTNPTIILVELSKKNNEISITLALSR 85
QY      61 KTTTLARNNLVYGVSDPENGKCRHYIFNDITSTERTDVENTLCCSSSSRVAMSIYNV 120
      86 -TTLVAVKNDLVYVAFDQVAG-KLRARVFPDISLATAKAIPPT-----AVQYQIGV 137
QY      121 NSLYPTMEKKAEVNSRNOVLOGIOLSSDICKISG---VDSFPVKTEAFELVLAIOVMSR 177
      138 TSNVYSIEGAAGSN-RVNFQDGFVKLEKEYMLANYGNVQDSRREARFLAIAIOMVAE 196
Db      178 AARFKYIENOVKTENRAFYPPPKVINLEEKWKCKISEAIIHNAKNGALPKPLELVDAKGTW 237
      197 AARFKYVESAIANN-----VYDPKYVSLNENMNSKISEGICRAKAKKVIISPTIELVNASNGK 252
QY      238 WIVLRVDEINRDVALLKYV 256
      253 WTVNVOVSDIKPDGILSYV 271
Db

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## RESULT 12

Q9A0E3 PRELIMINARY; PRT; 279 AA.



Db 138 PLEYEDYOSIEKNATTGDKSRKELGIDLISTIDKVNKKVRV-VKDEARFLLIGI 196  
QY 173 QMVSARAFKYIENOVKTENFNAFYPPDKYINLEEKWKISEAIIH-NAKNGALPK 226  
Db 197 QMSAEAVRFYIENLVTRNFPKKNSDNTYIOYOTSMGKISEAIIHSDCKNGKFNK 251

## RESULT 15

Q9S9E4 PRELIMINARY; PRT; 258 AA.  
AC Q9S9E4  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
DE rRNA-glycosidase (EC 3.2.2.22).  
OS Gelonium multiflorum (Euphorbiaceae himalayae).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Malpighiales; Euphorbiaceae; Gelonium.  
OX NCBI\_taxid=3979;  
RN (1)  
RP SEQUENCE.  
RX MEDLINE=96006751; PubMed=755324;  
RA Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,  
RT Toman P.D., Cheung L.;  
RT "Amino acid sequence analysis, gene construction, cloning, and  
expression of gelonin, a toxin derived from Gelonium multiflorum";  
RL J. Interferon Cytokine Res. 15:547-555(1995).  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
DR HSSP; P09989; IMRJ.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
KW Hydrolase; Toxin.  
SQ SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;

Query Match 23.7%; Score 321.5; DB 10; Length 258;  
Best Local Similarity 32.5%; Pred. No. 4,6e-19;  
Matches 86; Conservative 50; Mismatches 108; Indels 21; Gaps 8;

QY 2 INTITFDAGNATINKYATMESIRNQAKDPKLCYGIPLMLPTNSTPK-YLLVKGQANL 60  
Db 2 LDTVSFSTKGATYITVNFLELRVKKL-PEGNSHGIPLLRKGDDPGKCFVLVALSNDNG 60  
QY 61 KTTTLMLRRNNLYVMGSDPFNGNKKRYHIENDITSTE----RTDVENTLCSSSSRYA 115  
Db 61 QLAELAIIDVTSYVVGQ----VRNRSYFFKDPADPAAYEGLEFKNTIKNPLFLFGKTR-- 113  
QY 116 MSINYNSLYPTMEKKAENSRNOVQGIOLSSDIGKI--SGVDSFPVKTAEFFLLVAIO 173  
Db 114 --LHFGSGYPSLE--GEKAYRETTDGIETPLRIGIKKLDENAIQNKPTETIASLLVIO 169  
QY 174 MVSSEARFYIENOVKTENFNAFYPPDKYINLEEKWKISEAIIH-NAKNGALPKPLEYD 232  
Db 170 MVSSEARFYIENOVKTENFNAFYPPDKYINLEEKWKISEAIIH-NAKNGALPKPLEYD 232  
QY 233 AKGTKWIIVLRVDEINDVALLKYVN 257  
Db 230 ANGKKYIVTAVDQVKPKIALKFFVD 254

Search completed: July 2, 2003, 11:42:08  
Job time : 40.044 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 2, 2003, 11:40:38 ; Search time 23.917 Seconds  
(without alignments)  
738.742 Million cell updates/sec

Title: US-09-978-274A-6  
Perfect score: 793  
Sequence: 1 MINTTFDAGNATINKYATF.....SRNQVQLGIQLSSDICKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 11492915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PC1\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	793	100.0	154	10	US-09-978-274A-6
2	793	100.0	263	10	US-09-978-274A-4
3	788	99.4	314	10	US-09-978-274A-2
4	196.5	24.8	254	9	US-09-792-793A-85
5	196.5	24.8	327	9	US-09-792-793A-79
6	196.5	24.8	330	9	US-09-792-793A-82
7	196.5	24.8	332	9	US-09-792-793A-73
8	196.5	24.8	332	9	US-09-792-793A-76
9	191.5	24.1	275	9	US-09-792-793A-35
10	120	15.1	250	9	US-09-792-793A-36
11	111.5	14.1	247	9	US-09-792-793A-34
12	110.5	13.9	293	10	US-09-765-527-259
13	110.5	13.9	309	10	US-09-765-527-253
14	110.5	13.9	332	10	US-09-765-527-251
15	109.5	13.8	247	9	US-09-792-793A-39
16	109.5	13.8	251	10	US-09-765-527-247
17	89	11.2	252	10	US-09-347-064-2
18	89	11.2	252	10	US-09-347-064-8
19	87.5	11.0	325	9	US-09-792-793A-74

20	87.5	11.0	327	9	US-09-792-793A-75	Sequence 75, Appl
21	87	11.0	319	9	US-09-792-793A-38	Sequence 38, Appl
22	87	11.0	319	9	US-09-870-759-28	Sequence 28, Appl
23	87	11.0	694	10	US-09-334-477-49	Sequence 49, Appl
24	86	10.8	315	10	US-09-334-477-2	Sequence 2, Appl
25	86	10.8	323	10	US-09-334-477-21	Sequence 21, Appl
26	85	10.7	326	10	US-09-334-477-37	Sequence 37, Appl
27	85	10.7	690	10	US-09-334-477-47	Sequence 47, Appl
28	85	10.7	708	10	US-09-334-477-33	Sequence 33, Appl
29	82	10.3	247	9	US-09-792-793A-83	Sequence 83, Appl
30	82	10.3	249	9	US-09-792-793A-84	Sequence 84, Appl
31	82	10.3	293	9	US-09-792-793A-37	Sequence 37, Appl
32	82	10.3	320	9	US-09-792-793A-77	Sequence 77, Appl
33	82	10.3	322	9	US-09-792-793A-78	Sequence 78, Appl
34	82	10.3	323	9	US-09-792-793A-80	Sequence 80, Appl
35	82	10.3	325	9	US-09-792-793A-71	Sequence 71, Appl
36	82	10.3	325	9	US-09-792-793A-81	Sequence 81, Appl
37	82	10.3	327	9	US-09-792-793A-72	Sequence 72, Appl
38	80.5	10.2	1028	10	US-09-815-242-11516	Sequence 11516, A
39	78.5	9.9	318	10	US-09-334-477-6	Sequence 6, Appl
40	78.5	9.9	326	10	US-09-334-477-25	Sequence 25, Appl
41	78.5	9.9	329	10	US-09-334-477-39	Sequence 39, Appl
42	78.5	9.9	711	10	US-09-334-477-35	Sequence 35, Appl
43	75.5	9.5	761	9	US-09-895-913A-10	Sequence 10, Appl
44	73.5	9.3	1288	9	US-10-006-780-2	Sequence 2, Appl
45	71	9.0	889	9	US-09-952-267-15	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
US-09-978-274A-6  
Sequence 6, Application US/09978274A  
Patent No. US20020116737A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, Christopher  
APPLICANT: McPherson, Michael  
APPLICANT: Atkinson, Howard  
TITLE OF INVENTION: PLANT CELL DEATH SYSTEM  
FILE REFERENCE: 9341-028  
CURRENT FILING DATE: 2001-10-15  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 0025225.4  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 154  
TYPE: PRT  
ORGANISM: *Phytolacca americana*  
US-09-978-274A-6

Query Match 100.0%; Score 793; DB 10; Length 154;  
Best Local Similarity 100.0%; Pred. No. 1.3e-77;  
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MINTTFDAGNATINKYATFESLRNQAQKPLKCYGIMLPDPTNSTPYLLVKQAGNL 60  
|||||  
DB 1 MINTTFDAGNATINKYATFESLRNQAQKPLKCYGIMLPDPTNSTPYLLVKQAGNL 60  
|||||

QY 61 KTTTTLRRNNLYVWGYSDFPFGNCRVHIFNDISTERTDVENTLCSSSSRVAMSNY 120  
|||||  
DB 61 KTTTTLRRNNLYVWGYSDFPFGNCRVHIFNDISTERTDVENTLCSSSSRVAMSNY 120  
|||||

QY 121 NSLYPTMEKKAEVNSRNQVQLGIQLSSDICKIS 154  
|||||  
DB 121 NSLYPTMEKKAEVNSRNQVQLGIQLSSDICKIS 154  
|||||

RESULT 2  
US-09-978-274A-4

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: Sequence 4, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978,274A
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 4
: LENGTH: 263
: TYPE: PRF
: ORGANISM: Phytolacca americana
: US-09-978-274A-4
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Query Match          100.0%; Score 793; DB 10; Length 263;
Best Local Similarity 100.0%; Pred. No. 2,7e-77;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MINTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 60
DB 1 MINTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 60
QY 61 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 120
DB 61 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 120
QY 121 NSLYPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154
DB 121 NSLYPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154
```

```
RESULT 3
US-09-978-274A-2
: Sequence 2, Application US/09978274A
: Patent No. US20020116737A1
: GENERAL INFORMATION:
: APPLICANT: Thomas, Christopher
: APPLICANT: McPherson, Michael
: APPLICANT: Atkinson, Howard
: APPLICANT: Neelam, Anil
: TITLE OF INVENTION: PLANT CELL DEATH SYSTEM
: FILE REFERENCE: 9341-028
: CURRENT APPLICATION NUMBER: US/09/978,274A
: CURRENT FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: 0025225.4
: PRIOR FILING DATE: 2000-10-14
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 2
: LENGTH: 314
: TYPE: PRF
: ORGANISM: Phytolacca americana
: US-09-978-274A-2
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Query Match          99.4%; Score 788; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1,2e-76;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 61
DB 2 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 61
QY 25 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 84
DB 25 INTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 84
QY 62 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 121
DB 62 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 121
QY 85 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 144
DB 85 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 144
```

```
QY 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154
DB 145 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 177
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```
RESULT 4
US-09-792-793A-85
: Sequence 85, Application US/09792793A
: Patent No. US20020168370A1
: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Coggin, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 85
: LENGTH: 254
: TYPE: PRF
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Methionine-Saporin fusion
: US-09-792-793A-85
```

```
Query Match          24.8%; Score 196.5; DB 9; Length 254;
Best Local Similarity 31.9%; Pred. No. 3,6e-13;
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;
```

```
QY 1 MINTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 59
DB 1 MINTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 59
QY 60 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 118
DB 60 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 118
QY 61 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 115
DB 61 KITTLMLRRNNLYVWGSDPFGNKCRCYHIFNDITSTERTDVENTLSCSSSSRVAMSI 115
QY 119 NNSLYPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154
DB 119 NNSLYPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154
QY 116 EYTEDYOSIEKNAOITGDSQRKELGIDILSLTSMENVN 155
DB 116 EYTEDYOSIEKNAOITGDSQRKELGIDILSLTSMENVN 155
```

```
RESULT 5
US-09-792-793A-79
: Sequence 79, Application US/09792793A
: Patent No. US20020168370A1
: GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Coggin, Philip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 79
: LENGTH: 327
: TYPE: PRF
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion pro
: OTHER INFORMATION: 1-Beta-AM-SAPORIN
: US-09-792-793A-79
```

```
Query Match          24.8%; Score 196.5; DB 9; Length 327;
Best Local Similarity 31.9%; Pred. No. 5,1e-13;
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;
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```
QY 1 MINTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 59
DB 1 MINTTFDAGNATINKYATFMSLRNOAKDPKLCYGPMLPDTNSTPKYLLVKGANL 59
```

Db 74 MVTSTLTLVNPVPTAGQSSFDVKIRNNYKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 133  
QY 60 LKTTTLMRLNNLVYMGYSDFPENGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSI 118  
Db 134 -GTVSLGLKRDNLVYAVYLANDNTNVRAYFRSEITSAEST---ALFPETATNOKAL 188  
QY 119 NYSLYPTMEKKAEV---NSRNOVOIGIQLSSDICKIS 154  
Db 189 EYTEDYOSIEKNAOITOGDOSRKELGIDLDLSTSM EAVN 228

## RESULT 6

US-09-792-793A-82  
Sequence 82, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 82  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion prote  
US-09-792-793A-82

Query Match 24.8%, Score 196.5; DB 9; Length 330;  
Best Local Similarity 31.9%, Pred. No. 5.1e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTTFDAGNATINKYATFMSLRNQAOKDPKLCYGPMLPPTNSPKYLVLKLOGAN 59  
Db 77 MVTSTLTLVNPVPTAGQSSFDVKIRNNYKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 136  
QY 60 LKTTTLMRLNNLVYMGYSDFPENGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSI 118  
Db 137 -GTVSLGLKRDNLVYAVYLANDNTNVRAYFRSEITSAEST---ALFPETATNOKAL 191  
QY 119 NYSLYPTMEKKAEV---NSRNOVOIGIQLSSDICKIS 154  
Db 192 EYTEDYOSIEKNAOITOGDOSRKELGIDLDLSTSM EAVN 231

## RESULT 7

US-09-792-793A-73  
Sequence 73, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 73  
LENGTH: 332  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion prote  
US-09-792-793A-73

Query Match 24.8%, Score 196.5; DB 9; Length 332;  
Best Local Similarity 31.9%, Pred. No. 5.2e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTTFDAGNATINKYATFMSLRNQAOKDPKLCYGPMLPPTNSPKYLVLKLOGAN 59  
Db 79 MVTSTLTLVNPVPTAGQSSFDVKIRNNYKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 138  
QY 60 LKTTTLMRLNNLVYMGYSDFPENGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSI 118  
Db 139 -GTVSLGLKRDNLVYAVYLANDNTNVRAYFRSEITSAEST---ALFPETATNOKAL 193  
QY 119 NYSLYPTMEKKAEV---NSRNOVOIGIQLSSDICKIS 154  
Db 194 EYTEDYOSIEKNAOITOGDOSRKELGIDLDLSTSM EAVN 233

## RESULT 8

US-09-792-793A-76  
Sequence 76, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 76  
LENGTH: 332  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Chemokine-toxin fusion pr  
US-09-792-793A-76

Query Match 24.8%, Score 196.5; DB 9; Length 332;  
Best Local Similarity 31.9%, Pred. No. 5.2e-13;  
Matches 51; Conservative 37; Mismatches 61; Indels 11; Gaps 5;

QY 1 MINTTFDAGNATINKYATFMSLRNQAOKDPKLCYGPMLPPTNSPKYLVLKLOGAN 59  
Db 79 MVTSTLTLVNPVPTAGQSSFDVKIRNNYKDPNLKGTGTDIAVIGPPSKFKLRINFQSSR 138  
QY 60 LKTTTLMRLNNLVYMGYSDFPENGKCR-YHIFNDITSTERTDVENTLCSSSSRVAMSI 118  
Db 139 -GTVSLGLKRDNLVYAVYLANDNTNVRAYFRSEITSAEST---ALFPETATNOKAL 193  
QY 119 NYSLYPTMEKKAEV---NSRNOVOIGIQLSSDICKIS 154  
Db 194 EYTEDYOSIEKNAOITOGDOSRKELGIDLDLSTSM EAVN 233

## RESULT 9

US-09-792-793A-35  
Sequence 35, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: Mcdonald, John R.  
APPLICANT: Coggin, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 35

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; LENGTH: 275
; TYPE: PRT
; ORGANISM: Saponaria officinalis
US-09-792-793A-35

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Query Match	24.18;	Score 191.5;	DB 9;	Length 275;
Best Local Similarity	31.48;	Pred. No. 1.4e-12;		
Matches 50; Conservative	37;	Mismatches 61;	Indels 11;	Gaps 5

QY 2 INITITDAQNAIINKYATIMESILRNQADPKIKCGIDM-LPTDNPSPKLYLVLOQANL 60  
D 1 VNSITLDLVNPTACGYSSFEVDKIRNNVADPNLKYGTGFIAGICPPEKKEFLIRINQSSR- 59  
QY 61 KTTTLRLRNNTLYVAGSDPEFGNKCR-YHIFNDITTEPTDVENTLCSSSSSSVMSIN 119  
D 60 GTVSLGLKRDNLVYVAYLAMDMYNNRMYRRESEITSEST----ALPEPTTINQKALE 115  
QY 120 YNSLYPTMEKKAEV---NSRNOVLQGLISSLSDIGKIS 154  
D 116 YTEDVQSIENKAQITQGDGSRKELEGIDLLISTSEAVN 154

RESULT 10  
US-09-792-793A-36  
; Sequence 36, Application US/09792793A  
; Patent No. US2002016270A1

Query Match	15.1%	Score 120;	DB 9;	Length 250;
Best Local Similarity	28.8%;	Pred. No. 6e-05;		
Matches 44;	Conservative 26;	Mismatches 71;	Indels 12;	Gaps 7

OY	2 INTI --TFDGNATINTKRYATEMELESLNQAKDKRKYCGPMJPDNPSRPXYLLVLOCANL 60
Dd	4 LETIASLIDNNPT--TYSLFINIRTKVAADTEQC--TIQIKISKI--FQGRRSYIDLIIYST 59
OY	61 KITTLALRENNNIYVANGSDPFNGNCRXHINDITSTRTVENTLCCSSSRASRAMSINY 120
Dd	60 QKITLAIDMADLYVLGYSDIAN--NKGRAPFFRKDYEA---VAANNFPFGATGTNRILKTP 114
OY	121 NSLIYPPMEKKAEVNSRNVOVGCIOTLSSDIGKI 153
Dd	115 TGSYGDLKENGGLKRDN--PLGIIFRLXSIMYNI 145

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RESULT 11
US-09-792-793A-34
: Sequence 34, Application US/09792793A
: Patent No. US20020168370A1
:
GENERAL INFORMATION:
: APPLICANT: McDonald, John R.
: APPLICANT: Cogdins, Phillip
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
: TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
: FILE REFERENCE: 25020-601D
: CURRENT APPLICATION NUMBER: US/09/792,793A
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 93
:
SOFTWARE: Patentl Ver. 2.0

```

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; SEQ ID NO 34
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Bryonia dioica
US-09-792-793A-34

```

Query Match	14.1%	Score	11.5:	DB	9:	Length	247:
Best Local Similarity	26.8%	Pred. No.	0	00048:			
Matches	40:	Conservative	31:	Mismatches	61:	Indels	17:
						Gaps	7:

QY TTFDAQNAAIINKAATFMEELRNQAADPKCKGCEPMEDDT--NSPPKLVKLGQANAKTI 63  
Db VSRFLSGAATTSYGAFIKNLRL-EALPYRKYVINIPILLRSSISGSGRYTLHLTFYADETI 60  
QY TLELRNNLLVYNGASDPFGNKKCRHAFENDITSTERTVENTLSSSSSRVAM--SINYN 121  
Db 61 SVAVDVTNYINGY---LAGDVS--YFFNMSATF---AAKFVKKDAKKKVTLPYSNTE 112  
QY 122 SLVPTMEKKAENVNRNOVLGIQLSSDI 150  
Db 113 RL-----QTAACKIRKNIPUGLPAIDSAI 136

RESULT 12  
US-09-765-527-259  
; Sequence 259, Application US/09765527  
; Patent No. US20020006638A1

TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

```

? INFORMATION FOR SEQ ID NO:259:
? =====
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 293 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765,527-259

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Query Match	13.98;	Score 110.5;	DB 10;	Length 293;
Best Local Similarity	25.28;	Pred. No. 0.00078;		
Matches 39;	Conservative 29;	Mismatches 68;	Indels 19;	Gaps 6

```

QY      2 INTTFDAGNATINKYATFMESLRNQAKDPKLCYGPIMUPDTNSTPK--YLVLKLOGAN 59
      ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```



Db 24 LDTVSFSTKCATIYTYVNFLELRYKLGK-PEGNSHGIPLLRKKCDPGKCFVLAVALSDN 82  
QY 60 LKTTTLMLRRNNLYVMGYSDFPNNGKCRHYHFNIDITSTERDV-ENTLCSSSSSRVAMSI 118  
Db 83 GOLAEIADIVTSYVVGQ-----VRNRSYFFKDPADPAAYEGLEFKNT-----IKTRL 129  
QY 119 NYSNLYPTMEKKAVERNNOVOLGIQLSSDIGKI 153  
Db 130 HFGGTYPSE--GEKAYRETTDLGIEPLRIGIKKL 162

## RESULT 13

US-09-765-527-253  
Sequence 253, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 253:  
US-09-765-527-253

Query Match 13.9%; Score 110.5; DB 10; Length 309;  
Best Local Similarity 25.2%; Pred. No. 0.00084;  
Matches 39; Conservative 29; Mismatches 68; Indels 19; Gaps 6;

QY 2 INTTFDAGNATIKKYATFMESLRNQAOKPKLCYGPMLPTNSTPK--YLLVKLOGAN 59  
Db 24 LDTVSFSTKCATIYTYVNFLELRYKLGK-PEGNSHGIPLLRKKCDPGKCFVLAVALSDN 82  
QY 60 LKTTTLMLRRNNLYVMGYSDFPNNGKCRHYHFNIDITSTERDV-ENTLCSSSSSRVAMSI 118  
Db 83 GOLAEIADIVTSYVVGQ-----VRNRSYFFKDPADPAAYEGLEFKNT-----IKTRL 129  
QY 119 NYSNLYPTMEKKAVERNNOVOLGIQLSSDIGKI 153  
Db 130 HFGGTYPSE--GEKAYRETTDLGIEPLRIGIKKL 162

## RESULT 14

## US-09-765-527-251

Sequence 251, Application US/09765527  
Patent No. US20020006638A1  
GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/765,527  
FILING DATE: 18-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,803  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25,447  
REFERENCE/DOCKET NUMBER: 27129/33199  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 332 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 251:  
US-09-765-527-251

Query Match 13.9%; Score 110.5; DB 10; Length 332;  
Best Local Similarity 25.2%; Pred. No. 0.00092;  
Matches 39; Conservative 29; Mismatches 68; Indels 19; Gaps 6;

QY 2 INTTFDAGNATIKKYATFMESLRNQAOKPKLCYGPMLPTNSTPK--YLLVKLOGAN 59  
Db 24 LDTVSFSTKCATIYTYVNFLELRYKLGK-PEGNSHGIPLLRKKCDPGKCFVLAVALSDN 82  
QY 60 LKTTTLMLRRNNLYVMGYSDFPNNGKCRHYHFNIDITSTERDV-ENTLCSSSSSRVAMSI 118  
Db 83 GOLAEIADIVTSYVVGQ-----VRNRSYFFKDPADPAAYEGLEFKNT-----IKTRL 129  
QY 119 NYSNLYPTMEKKAVERNNOVOLGIQLSSDIGKI 153  
Db 130 HFGGTYPSE--GEKAYRETTDLGIEPLRIGIKKL 162

## RESULT 15

US-09-792-793A-39  
Sequence 39, Application US/09792793A  
Patent No. US20020168370A1  
GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93

;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 39  
;; LENGTH: 247  
;; TYPE: PRT  
;; ORGANISM: Trichosantheus kirlowii  
US-09-792-793A-39

Query Match 13.8%; Score 109.5; DB 9; Length 247;  
Best Local Similarity 27.8%; Pred. No. 0.00079;  
Matches 42; Conservative 29; Mismatches 59; Indels 21; Gaps 8;

OY 5 ITFDAGNATIKKATFMESLBNQAKDKLKCICIPMLPDTNSTP--KYLVLQGANLK 61  
DB 2 VSERLSGATSSSGVFISNR-KALPNERKLYDIPLL-RSLPGSORYALHLITNYADE 58  
OY 62 TITMLRRNNLYVAGYSDPFNGNRCRYHIFNDITSTERTDVENTLCSSSSSRVAM--SIN 119  
DB 59 TISVAIDVTNYINGYR--AGDTS--YFNEASATE--AAKYVFKDAMRKVTLPYISGN 110  
OY 120 YNSLYPTWEKKAENVSRNQVOLGIQILSSDI 150  
DB 111 YERL-----QTAAGKIRENIPGLPALDSAI 136

Search completed: July 2, 2003, 12:00:36  
Job time : 23.9717 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 2, 2003, 11:37:03 ; Search time 9.92767 Seconds  
(without alignments)  
456.414 Million cell updates/sec

Title: US-09-978-274A-6

Perfect score: 793  
Sequence: 1 MINTTFDAGNATINKYATF.....SRNOVOLGIQILSSDICKIS 154

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Bacillus.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	667.5	84.2	261	1	US-08-378-761A-9 Sequence 79, Appl
2	667.5	84.2	261	1	US-08-485-286-79 Sequence 79, Appl
3	667.5	84.2	261	1	US-08-488-113B-9 Sequence 9, Appl
4	667.5	84.2	261	1	US-08-477-484B-9 Sequence 9, Appl
5	667.5	84.2	261	2	US-08-646-360-9 Sequence 9, Appl
6	667.5	84.2	261	4	US-08-839-765-9 Sequence 9, Appl
7	667.5	84.2	261	4	US-09-136-389-9 Sequence 9, Appl
8	667.5	84.2	261	4	US-09-610-838-9 Sequence 9, Appl
9	660.5	83.3	261	1	US-07-901-707-9 Sequence 9, Appl
10	660.5	83.3	261	1	US-07-988-430-9 Sequence 9, Appl
11	660.5	83.3	261	1	US-08-425-336-9 Sequence 9, Appl
12	660.5	83.3	261	5	PCT-US92-09487-9 Sequence 9, Appl
13	596	75.2	313	1	US-08-373-858-2 Sequence 2, Appl
14	596	75.2	313	1	US-08-500-611-2 Sequence 2, Appl
15	596	75.2	313	4	US-08-500-694-2 Sequence 2, Appl
16	596	75.2	313	4	US-09-005-273-2 Sequence 2, Appl
17	596	75.2	313	4	US-08-501-253A-2 Sequence 2, Appl
18	596	75.2	313	5	PCT-US96-11546-2 Sequence 2, Appl
19	588	74.1	313	4	US-09-005-273-4 Sequence 4, Appl
20	463.5	58.4	305	1	US-08-138-636-2 Sequence 2, Appl
21	463.5	58.4	305	1	US-08-319-622A-2 Sequence 2, Appl
22	463.5	58.4	305	1	US-08-471-564-2 Sequence 2, Appl
23	191.5	24.1	259	1	US-07-901-707-10 Sequence 10, Appl
24	191.5	24.1	259	1	US-07-988-430-10 Sequence 10, Appl
25	191.5	24.1	259	1	US-08-425-336-10 Sequence 10, Appl
26	191.5	24.1	259	1	US-08-488-113B-10 Sequence 10, Appl
27	191.5	24.1	259	1	US-08-477-484B-10 Sequence 10, Appl

28	191.5	24.1	259	2	US-08-646-360-10 Sequence 10, Appl
29	191.5	24.1	259	4	US-08-839-765-10 Sequence 10, Appl
30	191.5	24.1	259	4	US-09-136-389-10 Sequence 10, Appl
31	191.5	24.1	259	4	US-09-610-838-10 Sequence 10, Appl
32	191.5	24.1	259	5	PCT-US92-09487-10 Sequence 10, Appl
33	191.5	24.1	260	1	US-08-378-761A-72 Sequence 72, Appl
34	191.5	24.1	260	1	US-08-485-286-72 Sequence 72, Appl
35	169	21.3	292	1	US-08-378-761A-81 Sequence 81, Appl
36	169	21.3	292	1	US-08-485-286-81 Sequence 81, Appl
37	120	15.1	250	1	US-07-901-707-8 Sequence 8, Appl
38	120	15.1	250	1	US-07-988-430-8 Sequence 8, Appl
39	120	15.1	250	1	US-08-425-336-8 Sequence 8, Appl
40	120	15.1	250	1	US-08-488-113B-8 Sequence 8, Appl
41	120	15.1	250	1	US-08-477-484B-8 Sequence 8, Appl
42	120	15.1	250	2	US-08-646-360-8 Sequence 8, Appl
43	120	15.1	250	4	US-08-839-765-8 Sequence 8, Appl
44	120	15.1	250	4	US-09-136-389-8 Sequence 8, Appl
45	120	15.1	250	4	US-09-610-838-8 Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-08-378-761A-79  
Sequence 79, Application US/08378761A  
Patent No. 5635384

#### GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESSES:  
ADDRESS: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-79

Query Match 84.2%; Score 667.5; DB 1: Length 261;

Best Local Similarity 85.6%; Pred. No. 2.2e-72;

Matches 131: Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 2 INTTFDAGNATINKYATFMSLRNOAKPKLCYGPMLPDTNSTPKYLLVKGANKL 61  
DB 1 INTTFDAGNATINKYATFMSLRNEAKDPKLCYGPMLPNTNSTITKYLKLOGASLK 60

QY	62	TTLMLRRNNLVYMGYSDFPENGKCRVHAFENDITSTETDVENTLCSSSSRVAMSYN	122
		.....   ..... ..   ...   ..	
Dd	61	TTLMLRRNNLVYMGYSDFPD-NKCRVHFIENDIKTEVSDENTLCPSNRVAAPLNYN	119
		.,	
QY	122	SLEPTMEKKAEVNSRNOVLGTQLTSSDGKIS	154
		.....   ..... ..   ...   ..	
Dd	120	GLEPTLEKRAGVTSRNEVOLGIQLTSSDGKIS	152

## RESULT 2

```

: US-08-485-286-79
: Sequence 79, Application US/08485286
: Patent No. 5646026
: Patent No. 5646026 5646119
: GENERAL INFORMATION:
: APPLICANT: WALSH, TERENCE A
: APPLICANT: HEY, TIMOTHY D
: APPLICANT: MORGAN, ALICE ER
: TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
: TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
: TITLE OF INVENTION: USING
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ANDREA T. BORUCKI
: STREET: 9330 ZIONSVILLE ROAD
: CITY: INDIANAPOLIS
: STATE: IN
: COUNTRY: US
: ZIP: 46268
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Releasee #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,286
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/378761
: FILING DATE: 26-JAN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: BORUCKI, ANDREA T
: REGISTRATION NUMBER: 33651
: REFERENCE/DOCKET NUMBER: 38272B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (317) 337-4846
: INFORMATION FOR SEQ ID NO: 79:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 261 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-485-286-79

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Query Match	84.2%	Score 667.5	DB 1:	Length 261:
Best Local Similarity	85.6%	Pred. No. 2.2e72:		
Matches 131:	Conservative 9:	Mismatches 12:	Indels 1:	Gaps 1
QY	2	INTITFDAGNATINKYATFMESLRNQAOKPFLKCYGIMLPDNTSPKYLVLVKGLOGANLK	61	
Db	1	INTITFDAGNATINKYATFMESLRNEADPSLCKGIMLPNTNTIYLLVLKLOGASLK	60	
QY	62	TITIMLRNNLYWGYSDPFNGKCRHIFENDITSTERTDVNTLCSSSSRFVAMISYNN	121	
Db	61	TITIMLRNNLYWGYSDPYD-NKCRHYHIFNDIKETESDVNTLCPSPNPRVAKPINYN	119	
QY	122	SLVPTMEKKAEVNSRNOYGLIOLSSIGKIS	154	
Db	120	GLVPTLEKKAGVTSRNEVGLIOLSSIGKIS	152	

RESULT 3  
US-08-488-113B-9  
; Sequence 9, Application US/08488113B  
; Patent No. 5744580

### RESULT 3

GENERAL INFORMATION:  
APPLICANT: Belter, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studolka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,113B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 110220US07/200-70.P3.C2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-113B-9

	Query Match	84.2%	Score 667.5	DB 1	Length 261
	Best Local Similarity	85.6%	Pred. No. 2.2e-72		
	Matches 131	Conservative 9	Mismatches 12	Indels 1	Gaps 1
QY	2 INTTFDAGNATINKYATFMESLRNQADPKYKCYGIMLPDNTSPRYLLVLLKLOGANLK 61				
Db	1 INTTFDAGNATINKYATFMESLRREADPSLKCYGIMLPNTSTIKYLLVLLKLOGASLK 60				
QY	62 TITMLRRNNLYVGVGSDPFNGKNCRIHIFNDITSEXTDVNTLCSSSSSRVAMSTNYN 121				
Db	61 TITMLRRNNLYVGVGSDPYD-NKCRHYHIFNDIKETESDVNTLCPSNRPRVAKPIYNN 119				
QY	122 SLPTMEKKAEVNSRNOVGLGIQLSSIGKIS 154				

DB 120 GLYPTLEKKAQVTSRNEVOLGIQLSSDIGKIS 152

## RESULT 4

US-08-477-484B-9  
Sequence 9, Application US/08477484B

Patent No. 5756699

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studinka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-484B-9

Query Match 84.2%; Score 667.5; DB 1; Length 261;

Best Local Similarity 85.6%; Pred. No. 2.2e-72;

Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 1 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 60

DB 122 SLVPTMEKKAQVTSRNEVOLGIQLSSDIGKIS 154

## RESULT 5

US-08-646-360-9  
Sequence 9, Application US/08646360

Patent No. 5837491

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studinka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-646-360-9

Query Match 84.2%; Score 667.5; DB 2; Length 261;

Best Local Similarity 85.6%; Pred. No. 2.2e-72;

Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

DB 2 INTITFDAGNATINKATFMSLRNQAQPKLKYGIPLPPTNSTIPKYLKLOGANLK 61

Db 61 TTTLRRNNLYVMGSDPYD-NKCRHYIFNDIKETESDVENTLCSSNPRVAKPINYN 119  
Qy 122 SLYPTMEKKAEVNSRNOVOLGIOLSSDICKIS 154  
120 GLYPTEKKAGVTSRNEVOLGIOLSSDICKIS 152

RESULT 6  
US-08-839-765-9  
Sequence 9, Application US/08839765  
Patent No. 6146631  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-9

Query Match 84.2%; Score 667.5; DB 4; Length 261;  
Best Local Similarity 85.6%; Pred. No. 2.2e-72;  
Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Qy 2 INTTFDGNATINNTATFMSLRNQADPKLCYGIPLPTNTSPKYLKLOGANLK 61  
Db 1 INTTFDGNATINNTATFMSLRNQADPKLCYGIPLPTNTSPKYLKLOGASLK 60

Qy 62 TTTLRRNNLYVMGSDPYD-NKCRHYIFNDIKETESDVENTLCSSSSRVAMSIYN 121  
Db 61 TTTLRRNNLYVMGSDPYD-NKCRHYIFNDIKETESDVENTLCSSNPRVAKPINYN 119  
Qy 122 SLYPTMEKKAEVNSRNOVOLGIOLSSDICKIS 154  
120 GLYPTEKKAGVTSRNEVOLGIOLSSDICKIS 152

RESULT 7  
US-09-136-389-9  
Sequence 9, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-9

Query Match 84.2%; Score 667.5; DB 4; Length 261;  
Best Local Similarity 85.6%; Pred. No. 2.2e-72;  
Matches 131; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

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OY      INITFDAGAAATINKATATMESLRNQAOKPKLCGIPMLPPTNSTPYLYLVKLOGAULK 61
Db      1 INITFDAGAAATINKATATMESLRNQAOKPKLCGIPMLPPTNSTPYLYLVKLOGAULK 60
OY      62 TITLMLRRNLVYMGSDPEFNGNCKRYHIFNDITSTERTDVENTLCSSSSRFVMSINYN 122
Db      61 TITLMLRRNLVYMGSDPYD-NKCRHYHFNDIKGREYSDVENTLCPSNPRVAPRIYVN 111
OY      122 SLPTMEKKAENVSRNQVLGIDILSSDGIKIS 154
Db      120 GLYPTLEKRAGYTSRNEVQLGIDILSSDGIKIS 152

RESULT 8
US-09-610-838-9
: Sequence 9, Application US/09610838
: Patent No. 6376217
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Studnka, Gary W.
: TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
: TITLE OF INVENTION: Proteins
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McAndrews, Heid & Malloy, Ltd.
: STREET: 500 West Madison Street, 34th floor
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60661

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/610,838
: FILING DATE: 06-JUL-2000
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/136,389
: FILING DATE: 18-AUG-1998
: APPLICATION NUMBER: 08/646,360
: FILING DATE: 13-MAY-1996
: APPLICATION NUMBER: PCT/US94/05348
: FILING DATE: 12-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/064,691
: FILING DATE: 12-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/988,430
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/901,707
: FILING DATE: 19-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/787,567
: FILING DATE: 04-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: McNicholas, Janet M.
: REGISTRATION NUMBER: 32,918
: REFERENCE/DOCKET NUMBER: 200-70, P4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/707-8889
: TELEFAX: 312/707-9155
: TELEX: 650 388-1248
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 261 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein

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[illegible]

Db 1 INTITFDGAGNATINKYATFMSLRNKAQDPKLCYGIPLPNTSTIKYLLVKGASLK 60  
Qy 62 TITLMLRRNNLYVMGYSDPENGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121  
Db 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKTEYSDVENTLCPSSNPRVAKPINYN 119  
Qy 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154  
Db 120 GLYPTLEKKAAGVTSRNEVOLGIQLSSKIGKIS 152

RESULT 10  
US-07-988-430-9  
Sequence 9, Application US/07988430  
Patent No. 5416202  
GENERAL INFORMATION:  
APPLICANT: Bernhard, Susan L.  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Lane, Julie A.  
APPLICANT: Lei, Shau-Ping  
TITLE OF INVENTION: Materials Comprising and Methods of  
Preparation and Use for Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/988,430  
FILING DATE: 19921209  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5416202and, Greta E.  
REGISTRATION NUMBER: 35302  
REFERENCE/DOCKET NUMBER: 31133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-988-430-9  
Query Match 83.3%, Score 660.5, DB 1, Length 261:  
Best Local Similarity 85.0%, Pred. No. 1.5e-71:  
Matches 130: Conservative 9, Mismatches 13, Indels 1, Gaps 1:  
Qy 2 INTITFDGAGNATINKYATFMSLRNKAQDPKLCYGIPLPNTSTIKYLLVKGASLK 61  
Db 1 INTITFDGAGNATINKYATFMSLRNKAQDPKLCYGIPLPNTSTIKYLLVKGASLK 60

Qy 62 TITLMLRRNNLYVMGYSDPENGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121  
Db 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKTEYSDVENTLCPSSNPRVAKPINYN 119  
Qy 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154  
Db 120 GLYPTLEKKAAGVTSRNEVOLGIQLSSKIGKIS 152

RESULT 11  
US-08-425-336-9  
Sequence 9, Application US/08425336  
Patent No. 5621083  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
Proteins  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,336  
FILING DATE: 18-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 31394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acid  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-425-336-9

Query Match 83.3%, Score 660.5, DB 1, Length 261:  
Best Local Similarity 85.0%, Pred. No. 1.5e-71:  
Matches 130: Conservative 9, Mismatches 13, Indels 1, Gaps 1:  
Qy 2 INTITFDGAGNATINKYATFMSLRNKAQDPKLCYGIPLPNTSTIKYLLVKGASLK 61  
Db 1 INTITFDGAGNATINKYATFMSLRNKAQDPKLCYGIPLPNTSTIKYLLVKGASLK 60  
Qy 62 TITLMLRRNNLYVMGYSDPENGKCRHYHFNIDTSTERTDVENTLCSSSSRVAMSINYN 121  
Db 61 TITLMLRRNNLYVMGYSDPYD-NKCRHYHFNIDIKTEYSDVENTLCPSSNPRVAKPINYN 119  
Qy 122 SLVPTMEKKAEVNSRNOVOLGIQLSSDICKIS 154



Db 120 GLYPTLEKKAAGVTSRNEVQIGIQLISKIGKIS 152

## RESULT 12

PCT-US92-09487-9

Sequence 9, Application PC/TUS9209487

GENERAL INFORMATION:

APPLICANT: Bernhard, Susan L.

APPLICANT: Belter, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Lane, Julie A.

APPLICANT: Lei, Shau-Ping

TITLE OF INVENTION: Materials Comprising and Methods of

PREPARATION AND USE FOR RIBOSOME-INACTIVATING PROTEINS

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09487

FILING DATE: 19921104

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.

REGISTRATION NUMBER: 35302

REFERENCE/DOCKET NUMBER: 31133

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3836

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-09487-9

Query Match

Best Local Similarity 83.3%; Score 660.5; DB 5; length 261;

Matches 130; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

2 INTTFDAGNATINKYATFMSLRNOADPKLCYGIPLDPTNSTPKYLLVKGLOGANLK 61

1 INTTFDAGNATINKYATFMSLRNEADPKLCYGIPLDPTNSTPKYLLVKGLOGASLK 60

62 TITLMLRNNILVYMGYSDFPFGNCRHYIFNDITSTERTDVENTLSCSSSRVAMSIYN 121

61 TITLMLRNNILVYMGYSDFPD-NKCRHYIFNDIKGTESDVENLTCPSSNPRVAKPIYN 119

122 SLVPTMEKKAEVNSRNOVQIGIQLISDICKIS 154

120 GLYPTLEKKAAGVTSRNEVQIGIQLISKIGKIS 152

RESULT 13

US-08-373-858-2

Sequence 2, Application US/08373858

Patent No. 5633155

GENERAL INFORMATION:

APPLICANT: Kim, Man-Keun

APPLICANT: Lee, Kwan-Ho

APPLICANT: Na, Byeong-Kook

APPLICANT: Jeong, Han-Seung

APPLICANT: Choi, Kyu-Whan

APPLICANT: Moon, Young-Ho

APPLICANT: Jeon, Hong-Seob

TITLE OF INVENTION: Expression Vector for Phyto

TITLE OF INVENTION: Antiviral Protein and Process for Preparing Transgenic

TITLE OF INVENTION: Plant Transformed Thereof.

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: US

ZIP: 10022-7513

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,858

FILING DATE: 18-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Peter

REGISTRATION NUMBER: 25,351

REFERENCE/DOCKET NUMBER: 0136/17986-US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7770

TELEFAX: 212-753-6237

TELEX: 236687

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Phyto

TISSUE TYPE: Leaf

US-08-373-858-2

Query Match

Best Local Similarity 75.2%; Score 596; DB 1; length 313;

Matches 110; Conservative 23; Mismatches 20; Indels 0; Gaps 0;

2 INTTFDAGNATINKYATFMSLRNOADPKLCYGIPLDPTNSTPKYLLVKGLOGANLK 61

23 VNTIIVNGSTTISKYATFLNDRNEADPKLCYGIPLDPTNSTPKYLLVKGLOGANLK 82

62 TITLMLRNNILVYMGYSDFPFGNCRHYIFNDITSTERTDVENTLSCSSSRVAMSIYN 121

83 TITLMLRNNILVYMGYSDFPFGNCRHYIFNDITSTERTDVENTLSCSSSRVAMSIYN 142

122 SLVPTMEKKAEVNSRNOVQIGIQLISDICKIS 154

143 SRVPTLEKKAAGVTSRNOVQIGIQLISDICKIS 175

RESULT 14

US-08-500-611-2

Sequence 2, Application US/08500611

US-08-500-611-2

Dh 143 S

Job time : 9.92767 secs